STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 94446

TO: Christine Saoud **Location:** **Art Unit: 1647** **May 30, 2003** **Case Serial Number: 901938**	**From: P. Sheppard** **Location: CM1-1E03** **Phone: (703) 308-4499** **sheppard@uspto.gov**

10B19

Search Notes

[redacted]TIC-Biotech/Ch mLib

94446

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From: Saoud, Christine
Sent: Tuesday, May 20, 2003 10:35 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

09/901,938

Please search SEQ ID NO:1 and 2 in the patent and commercial databases (no interference, please).

Thank you,

Christine Saoud
A.U. 1647
CM1 - 10E03
305-7519
mailbox in 10B19

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_____	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_____	Bibliographic:_____	DRLink:_____
Date Completed: 5/30/03	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_____
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 404 Seconds
(without alignments)
8985.696 Million cell updates/sec

Title: US-09-901-938-1
Perfect score: 1612
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1612	100.0	1612	24	ABK48318	cDNA encoding huma
2	1598	99.1	2770	24	ABL50577	Human OST311 polyn
3	1256	77.9	2749	21	AAC61157	Human fibroblast g
4	1238.4	76.8	1240	22	AAH64781	Human secreted pro
5	1211	75.1	1211	22	AAH28133	Nucleotide sequenc
6	1211	75.1	1211	24	ABA97195	Human zFGF12 encod
7	1151	71.4	13200	24	ABL50582	Human OST311 genom
8	912	56.6	1973	21	AAC61159	Human fibroblast g
9	798	49.5	996	22	AAS21376	Human cDNA sequenc
10	798	49.5	996	22	AAF44266	Human PRO9828 nucl
11	756	46.9	756	22	AAD16366	Human sbgFGF-19b g
12	756	46.9	756	22	AAH75021	Nucleotide sequenc
13	756	46.9	756	22	AAH75033	Nucleotide sequenc
14	756	46.9	756	24	ABN81575	Human FGF23 protei
15	756	46.9	756	24	ABL91738	Human polynucleoti
16	753	46.7	753	22	AAH76317	Human fibroblast g
17	685.6	42.5	747	24	ABL50653	His-OST311 DNA seq
18	684	42.4	684	24	ABL50578	Human OST311 polyn
19	674.4	41.8	690	24	ABL50654	MK-OST311 DNA sequ
20	659.2	40.9	805	21	AAC61155	Monkey fibroblast
21	537	33.3	537	21	AAC61158	Human fibroblast g
22	534	33.1	534	21	AAC61160	Human fibroblast g
23	528	32.8	753	22	AAH28134	Degenerate sequenc
24	528	32.8	753	24	ABA97196	Human zFGF12 degen
25	493.2	30.6	531	21	AAC61156	Monkey fibroblast
26	465	28.8	465	24	ABL50579	Human OST311 polyn
27	457.4	28.4	1559	24	ABK48319	cDNA encoding mous
28	428	26.6	756	22	AAH75022	Nucleotide sequenc
29	428	26.6	756	22	AAH75032	Nucleotide sequenc
30	293.4	18.2	543	24	ABL50581	Mouse OST311 polyn
31	219	13.6	219	24	ABL50580	Human OST311 polyn
32	74	4.6	630	22	AAF89921	Nucleotide sequenc
33	73.2	4.5	624	22	AAD09152	Human fibroblast g
34	72.8	4.5	514	22	AAF76715	Human fibroblast g
35	72.6	4.5	651	24	ABL91719	Human polynucleoti
36	72.6	4.5	2133	20	AAX52224	Protein PRO533 cDN
37	72.6	4.5	2133	20	AAX28430	FGF homologue PRO5
38	72.6	4.5	2137	20	AAV72455	Human PRO533 cDNA.
39	72.6	4.5	2137	21	AAC58599	Human PRO533 prote
40	72.6	4.5	2137	21	AAA30028	Human PRO533 nucle
41	72.6	4.5	2137	22	AAF58498	PRO533 coding sequ
42	72.6	4.5	2137	22	AAC87022	Nucleotide sequenc
43	72.6	4.5	2137	22	AAF72382	Human PRO533 cDNA.
44	72.6	4.5	2137	24	ABL95599	Human angiogenesis
45	72.6	4.5	2137	24	ABL88110	Human PRO533 cDNA

ALIGNMENTS

RESULT 1
ABK48318
ID ABK48318 standard; cDNA; 1612 BP.
XX
AC ABK48318;
XX
DT 02-JUL-2002 (first entry)
XX
DE cDNA encoding human fibroblast growth factor-23 (FGF23).
XX
KW Fibroblast growth factor 23; FGF23; hypophosphataemic disorder;
KW autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;
KW X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia;
KW TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH;
KW hypophosphataemic bone disease; HBD; epidermal nevus syndrome;
KW nephrolithiasis; hyperphosphataemic disorder; mild renal insufficiency;
KW tumoural calcinosis; osteoporosis; dermatomyositis; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 147..902
FT /*tag= a
FT /product= "FGF23"
FT /note= "Fibroblast growth factor 23"
FT sig_peptide 147..218
FT /*tag= b
FT mat_peptide 219..899
FT /*tag= c
FT /label= "Mature_FGF23"
XX
PN WO200208271-A1.

XX
PD 31-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US21738.
XX
PR 19-JUL-2000; 2000US-219137P.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
XX
PI Econs M, White K, Strom TM, Meitinger T;
XX
DR WPI; 2002-329399/36.
DR P-PSDB; AAU79355.
XX
PT Novel fibroblast growth factor 23, and polynucleotides encoding the
PT polypeptides, useful for treating hyperphosphataemic disorders such as
PT mild renal insufficiency or tumoural calcinosis, or coronary artery
PT disease -
XX
PS Claim 2; Fig 5A; 130pp; English.
XX
CC The invention describes an isolated polypeptide (I) comprising a
CC fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
CC homologue or fragment. (I) is useful for treatment of a hypophosphataemic
CC disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
CC X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic
CC rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD),
CC epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
CC (TIO), and nephrolithiasis. (I) can also be used in treatment of a
CC hyperphosphataemic disorder such as mild renal insufficiency and tumoural
CC calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
CC deposition of calcium and phosphate in the arteries or soft tissues of
CC mammal, coronary artery disease may also be treated using methods
CC described in the invention. Preferably, the nucleic acid or the
CC polypeptide comprises a mutation that confers increased stability on
CC FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene
CC therapy to treat diseased individuals. This sequence encodes the novel
CC human fibroblast growth factor 23 (FGF23) studied in the invention.
XX
SQ Sequence 1612 BP; 405 A; 462 C; 418 G; 327 T; 0 other;

Query Match 100.0%; Score 1612; DB 24; Length 1612;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 AAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCA 120

Qy     121 GCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTG 180
Db     121 GCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTG 180

Qy     181 CCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGC 240
Db     181 CCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGC 240

Qy     241 TCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACC 300
Db     241 TCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACC 300

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Qy     421 GATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGA 480
Db     421 GATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGA 480

Qy     481 ACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGT 540
Db     481 ACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGT 540

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Qy     661 CCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACG 720
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Qy     841 TGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCCTTCGCCAAGTTCATCT 900
Db     841 TGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCT 900

Qy     901 AGGGTCGCTGGAAGGGCACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAG 960
Db     901 AGGGTCGCTGGAAGGGCACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAG 960

Qy     961 GACCAGGTCCCTTGACGTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGC 1020
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Qy    1021 TGCTTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGT 1080
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Qy    1081 CATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCA 1140
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Qy    1141 ACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATA 1200
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Qy    1201 TTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAA 1260
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Qy    1321 AATCGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCC 1380
Db    1321 AATCGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCC 1380

Qy    1381 CACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAA 1440
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Qy    1441 ACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGAC 1500
Db    1441 ACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGAC 1500
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RESULT 2
ABL50577
ID   ABL50577 standard; cDNA; 2770 BP.
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AC   ABL50577;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Human OST311 polynucleotide sequence SEQ ID NO:1.
XX
KW   OST311; phosphoric acid metabolism; calcium metabolism; calcification;
KW   vitamin D metabolism; hypophosphataemia; phosphate transport; cytostatic;
KW   chromosome 12p13; osteopathic; nephrotropic; antihyperphosphataemic;
KW   phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
KW   bone formation abnormality; vitamin D resistance; Paget's disease;
KW   bone calcium deficiency; kidney disorder; kidney function deficiency;
KW   renal phosphate leakage; urinary tubule acidosis; Fanconi's disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200214504-A1.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-JP06944.
XX
PR   11-AUG-2000; 2000JP-0245144.
PR   21-SEP-2000; 2000JP-0287684.
PR   22-DEC-2000; 2000JP-0391077.
PR   19-APR-2001; 2001JP-0121527.
XX
PA   (KIRI ) KIRIN BEER KK.
XX
PI   Yamashita T,  Shimada T,  Mizutani S,  Fukumoto S;
XX
DR   WPI; 2002-227350/28.
DR   P-PSDB; ABB06940.
XX
PT   Polypeptides useful for regulating phosphate transport and calcium
PT   metabolism and DNA encoding them for treatment of phosphate and calcium
PT   metabolism disorders, including bone formation abnormalities and kidney
PT   diseases -
XX
PS   Claim 2; Page 153-157; 221pp; Japanese.
XX
CC   The present invention describes DNA encoding a polypeptide having the
CC   activities of inhibiting hypophosphataemia, phosphate transport and
CC   calcification, and regulating vitamin D metabolism in vivo. The
CC   polypeptide is of human origin (designated OST311) which is localised to
CC   chromosome 12p13, or is derived from this by addition, deletion and/or
CC   substitution of one or more amino acid residues. OST311 has osteopathic,
CC   nephrotropic, antihyperphosphataemic and cytostatic activities. The
CC   OST311 polypeptide regulates phosphorus transport and calcium metabolism.
CC   OST311 sequences can be used for the treatment and diagnosis of skeletal
CC   disorders such as bone cancer, bone formation abnormalities, vitamin D
CC   resistance, osteoporosis, Paget's disease and bone calcium deficiency;
CC   kidney disorders such as kidney function deficiency, renal phosphate
CC   leakage, urinary tubule acidosis and Fanconi's disease. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 2770 BP; 727 A; 704 C; 630 G; 709 T; 0 other;

  Query Match             99.1%;  Score 1598;  DB 24;  Length 2770;
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Qy     75 GCCTGGGCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCA 134
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Qy    495 CACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTC 554
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Qy    555 AGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAG 614
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Qy    855 GGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAG 914
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Db    841 GGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAG 900

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Db    901 GGCACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTG 960

Qy    975 ACGTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGT 1034
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Qy   1035 CCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACC 1094
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```
Db    1021 CCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACC 1080

Qy    1095 GCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGA 1154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGA 1140

Qy    1155 AATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGT 1214
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGT 1200

Qy    1215 GCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1260

Qy    1275 GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCA 1334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCA 1320

Qy    1335 GAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAG 1394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAG 1380

Qy    1395 TGTGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAAACACTACTTTCAAG 1454
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TGTGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAAACACTACTTTCAAG 1440

Qy    1455 CCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGG 1514
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGG 1500

Qy    1515 TGAAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAATAGAAAA 1574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGAAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAATAGAAAA 1560

Qy    1575 CTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1612
           |||||||||||||||||||||||||||||||||||||
Db    1561 CTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1598
```

RESULT 3
AAC61157
ID AAC61157 standard; cDNA; 2749 BP.
XX
AC AAC61157;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human fibroblast growth factor-20 (FGF-20) cDNA sequence.
XX
KW Fibroblast growth factor-20; FGF-20; cytostatic; nootropic; metastasis;
KW neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer;
KW leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease;
KW neurodegenerative disorder; Parkinson's disease; multiple sclerosis;
KW amylotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy;
KW Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder;
KW haematopoietic disorder; myeloproliferative disorder; human; ss.
XX
OS Homo sapiens.
XX
PN WO200060085-A1.
XX
PD 12-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US08076.
XX
PR 02-APR-1999; 99US-0127534.
PR 03-DEC-1999; 99US-0454470.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ, Wrighton NC;
XX
DR WPI; 2000-647346/62.
DR P-PSDB; AAY85638.
XX
PT Novel nucleic acids encoding fibroblast growth factor-20, useful for
PT detecting and modulating FGF-20 and for treating, e.g. cancer,
PT neurodegenerative disorders, hepatic disorders and cardiovascular
PT disorders -
XX
PS Claim 1; Fig 9; 149pp; English.
XX
CC Polynucleotide sequences AAC61155-C61160 encode fibroblast growth
CC factor-20 (FGF-20) proteins AAY85637-Y85639. The invention includes
CC FGF-20 sequences isolated from humans and monkeys. Proteins,
CC polynucleotides, agonists and antagonists of the invention have
CC cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant
CC and hepatotropic activity. The peptides, nucleotides and their binding
CC agents my be used to modulate the expression or activity of FGF-20, or to
CC diagnose aberrant FGF-20 expression. FGF20 activity or expression may be
CC down-regulated to treat proliferative or differentiative disorders (e.g.
CC cancers and leukaemia), tumour angiogenesis and metastasis, skeletal
CC dysplasia, neurodegenerative disorders (e.g. Alzheimer's disease,
CC Parkinson's disease, multiple sclerosis, amylotrophic lateral sclerosis,
CC progressive supranuclear palsy, epilepsy or Creutzfeldt-Jakob disease),
CC hepatic disorders, cardiovascular disorders and haematopoietic and/or
CC myeloproliferative disorders.
XX
SQ Sequence 2749 BP; 747 A; 645 C; 633 G; 724 T; 0 other;

Query Match 77.9%; Score 1256; DB 21; Length 2749;
Best Local Similarity 98.1%; Pred. No. 5.5e-293;
Matches 1271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy     317 GAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATC 376
           | ||||| ||| | | | || | | |||||||||||||||||||
Db     277 GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATAGGTGCCCTGATGATCAGATC 336

Qy     377 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 396

Qy     437 TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     397 TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA 456

Qy     497 CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG 516

Qy     557 TCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     517 TCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTT 576

Qy     617 CCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCA 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     577 CCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCA 636

Qy     677 CACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGC 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     637 CACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGC 696

Qy     737 CCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAG 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     697 CCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAG 756

Qy     797 CCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGG 856
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     757 CCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGG 816

Qy     857 GGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG 916
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     817 GGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG 876

Qy     917 CACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGAC 976
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    877 CACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGAC 936

Qy    977 GTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCC 1036
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 GTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCC 996

Qy   1037 CTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGC 1096
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 CTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGC 1056

Qy   1097 CTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAA 1156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 CTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAA 1116

Qy   1157 TTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGC 1216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 TTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGC 1176

Qy   1217 CTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGC 1276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 CTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGC 1236

Qy   1277 AGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCAGA 1336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 AGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCAGA 1296

Qy   1337 AGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAGTG 1396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 AGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAGTG 1356

Qy   1397 TGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAAACACTACTTTCAAGCC 1456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 TGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAAACACTACTTTCAAGCC 1416

Qy   1457 TTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTG 1516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 TTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTG 1476

Qy   1517 AAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAATAGAAAACT 1576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 AAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAATAGAAAACT 1536

Qy   1577 CAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1612
          |||||||||||||||||||||||||||||||||||
Db   1537 CAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1572
```

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RESULT 4
AAH64781
ID   AAH64781 standard; cDNA; 1240 BP.
XX
AC   AAH64781;
XX
DT   11-SEP-2001  (first entry)
XX
DE   Human secreted protein cDNA, SEQ ID NO: 57.
XX
KW   Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW   GENSET; ss.
XX
OS   Homo sapiens.
XX
PN   WO200142451-A2.
XX
PD   14-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-IB01938.
XX
PR   08-DEC-1999;   99US-0169629.
PR   06-MAR-2000; 2000US-0187470.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Bougueleret L,  Jobert S;
XX
DR   WPI; 2001-367870/38.
DR   P-PSDB; AAG89178.
XX
PT   Full length GENSET human nucleic acids encoding potentially secreted
PT   proteins, useful in gene therapy and vaccination against a variety of
PT   diseases, and for diagnosis of those diseases -
XX
PS   Claim 7; Page 622-623; 921pp; English.
XX
CC   The invention relates to full length GENSET human nucleic acids encoding
CC   potentially secreted proteins. The nucleic acids and the polypeptides
CC   they encode may be used in the prevention, treatment and diagnosis of
CC   diseases associated with inappropriate GENSET gene expression. For
CC   example, they be used to treat disorders associated with decreased
CC   GENSET gene expression by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of GENSET or by supplementing
CC   the patients own production of GENSET polypeptides. Conversely,
CC   antisense nucleic acid molecules may be administered to down regulate
CC   GENSET expression by binding with the cells' own genes and preventing
CC   their expression. The sense and antisense nucleic acids may also be
CC   used as DNA probes in diagnostic assays to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples, and hence to
CC   determine which patients may be in need of restorative therapy.
CC   The GENSET polypeptides may be used as antigens in the production of
CC   antibodies and in assays to identify modulators (agonists and
CC   antagonists) of GENSET polypeptide expression and activity. The
CC   present sequence is a GENSET nucleic acid of the invention.
XX
SQ   Sequence 1240 BP; 292 A; 383 C; 325 G; 240 T; 0 other;
```

Query Match 76.8%; Score 1238.4; DB 22; Length 1240;
Best Local Similarity 99.9%; Pred. No. 7e-289;
Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     21 AGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGG 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGG 60

Qy     81 GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG 120

Qy    141 GGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC 180

Qy    201 ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC 240

Qy    261 CTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAAT 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAAT 300

Qy    321 GGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAG 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAG 360

Qy    381 GATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTC 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTC 420

Qy    441 AGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAG 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAG 480

Qy    501 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 540

Qy    561 GGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTG 620
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTG 600

Qy    621 TCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACC 680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACC 660

Qy    681 CGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGG 740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGG 720

Qy    741 ATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCG 800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCG 780

Qy    801 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 840

Qy    861 ACGGGCCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 900

Qy    921 CTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC 980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC 960

Qy    981 CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTC 1040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTC 1020

Qy   1041 CACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTC 1100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTC 1080

Qy   1101 CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC 1160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC 1140

Qy   1161 CCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCT 1220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCT 1200

Qy   1221 CCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAA 1260
                |||||||||||||||||||| ||||||||||||||||
Db   1201 CCTCTTTATCACTTTTAAGCATGAAAAAAAAAAAAAAAAA 1240
```

RESULT 5
AAH28133
ID AAH28133 standard; DNA; 1211 BP.
XX
AC AAH28133;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of fibroblast growth factor homologue zFGF12.
XX
KW Fibroblast growth factor; FGF; zFGF12; chromosome 12; 12q.1.3;
KW neuronal cell; prostatic cell; pancreatic cell; haematopoietic cell;
KW hyperplasia; regeneration; diabetes; amylotrophic lateral sclerosis;
KW stroke; angiogenesis; wound healing; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   115..870
FT   /*tag= a
FT   /product= "fibroblast growth factor homologue zFGF12"
FT sig_peptide   115..186
FT   /*tag= b
FT mat_peptide   187..870
FT   /*tag= c
XX
PN WO200149740-A1.
XX
PD 12-JUL-2001.
XX
PF 04-JAN-2001; 2001WO-US00238.
XX
PR 05-JAN-2000; 2000US-0478062.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC;
XX
DR WPI; 2001-418357/44.
DR P-PSDB; AAB84652.
XX
PT A fibroblast growth factor homolog polypeptide zFGF12 and the nucleic
PT acids that encode it, useful for preventing, diagnosing and controlling
PT e.g. diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis
PT and wound healing -
XX
PS Claim 16; Page 58-60; 66pp; English.
XX
CC The present sequence encodes a human fibroblast growth factor (FGF)
CC homologue, designated zFGF12. The zFGF12 polypeptides contain a motif
CC (see AAB84654) that occurs in all known members of the FGF family, which
CC is unique to these proteins. This motif is highly conserved in all
CC members of the FGF family, however, zFGF12 appears to be unique in that
CC the conserved Glu is a His (residue 117) substituting a basic amino
CC acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped
CC to chromosome 12, location 12q.1.3. zFGF12 may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate FGF expression. Disorders and processes that may be
CC prevented, diagnosed, and treated include, for example proliferation
CC of neuronal, prostatic and pancreatic tissue cells, growth and
CC differentiation of haematopoietic cells, hyperplasia and regeneration,
CC diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis and
CC wound healing.
XX
SQ Sequence 1211 BP; 273 A; 380 C; 321 G; 237 T; 0 other;

Query Match 75.1%; Score 1211; DB 22; Length 1211;
Best Local Similarity 100.0%; Pred. No. 2.8e-282;
Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     33 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 60

Qy     93 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 120

Qy    153 GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC 180

Qy    213 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 240

Qy    273 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 300

Qy    333 GGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT 360

Qy    393 GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATT 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATT 420
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Qy     453 TTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAC 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAC 480

Qy     513 GGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAG 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAG 540

Qy     573 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 600

Qy     633 GAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAG 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAG 660

Qy     693 GACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCC 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCC 720

Qy     753 CCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGAC 812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGAC 780

Qy     813 CCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAA 872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAA 840

Qy     873 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 900

Qy     933 TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA 992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA 960

Qy     993 AGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC 1052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC 1020

Qy    1053 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1080

Qy    1113 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1172
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1140

Qy    1173 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1200

Qy    1233 TTTTAAGCATA 1243
           |||||||||||
Db    1201 TTTTAAGCATA 1211
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```
RESULT 6
ABA97195
ID   ABA97195 standard; DNA; 1211 BP.
XX
AC   ABA97195;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human zFGF12 encoding sequence.
XX
KW   zFGF12; human; fibroblast growth factor; FGF; vulnerary; chemotherapy;
KW   lung injury; epithelial cell; mesenchymal cell; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             115..870
FT                   /*tag=  a
FT                   /product= "zFGF12"
FT   sig_peptide     115..186
FT                   /*tag=  b
FT                   /label= secretory_signal_sequence
FT   mat_peptide     187..867
FT                   /*tag=  c
FT                   /product= "mature_zFGF12"
XX
PN   US2001044525-A1.
XX
PD   22-NOV-2001.
XX
PF   04-JAN-2001; 2001US-0754634.
XX
PR   05-JAN-2000; 2000US-174582P.
XX
PA   (CONK/) CONKLIN D C.
XX
PI   Conklin DC;
XX
DR   WPI; 2002-105575/14.
DR   P-PSDB; ABB08352.
XX
PT   New fibroblast growth factor, designated zFGF12 is for promoting wound
PT   healing, protecting and stimulating epithelial cells after chemotherapy
PT   or radiation, and stimulating lung epithelial cells after premature
PT   birth or injury  -
XX
PS   Claim 16; Page 21-22; 34pp; English.
XX
CC   The invention relates to a fibroblast growth factor polypeptide,
CC   designated zFGF12, comprising a sequence at least 95 % identical to
CC   residues 25 to 251 of the 251 amino acid sequence, given in the
CC   specification. The activity of the fibroblast growth factor of the
CC   invention may be described as vulnerary. zFGF12 can be used to promote
CC   wound healing of the epidermis, to protect and promote recovery of
CC   epithelial cells in the gastrointestinal tract, small intestine and oral
CC   mucosa after chemotherapy or radiation, and to stimulate lung epithelial
CC   cells after lung injury or complications in neonates following premature
CC   birth. The polypeptide can also be used to modulate proliferation and
CC   function of epithelial cells of prostate, cornea, mammary and kidney
CC   tissue. The polypeptide is also useful to stimulate proliferation of
CC   cultured mesenchymal cells and to identify new family members. The
CC   current sequence represents the human zFGF12 encoding sequence.
XX
SQ   Sequence 1211 BP; 273 A; 380 C; 321 G; 237 T; 0 other;
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  Query Match             75.1%;  Score 1211;  DB 24;  Length 1211;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-282;
  Matches 1211;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 92
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 60

Qy      93 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 120

Qy     153 GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC 180

Qy     213 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 240

Qy     273 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 300
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Qy    333 GGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT 360

Qy    393 GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATT 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATT 420

Qy    453 TTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAC 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAC 480

Qy    513 GGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAG 540

Qy    573 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 600

Qy    633 GAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAG 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAG 660

Qy    693 GACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCC 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCC 720

Qy    753 CCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGAC 812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGAC 780

Qy    813 CCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAA 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAA 840

Qy    873 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 900

Qy    933 TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA 992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA 960

Qy    993 AGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC 1020

Qy   1053 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1080

Qy   1113 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1140

Qy   1173 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1200

Qy   1233 TTTTAAGCATA 1243
          ||||||||||||
Db   1201 TTTTAAGCATA 1211
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RESULT 7
ABL50582
ID   ABL50582 standard; DNA; 13200 BP.
XX
AC   ABL50582;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Human OST311 genomic DNA 12p13 SEQ ID NO:11.
XX
KW   OST311; phosphoric acid metabolism; calcium metabolism; calcification;
KW   vitamin D metabolism; hypophosphataemia; phosphate transport; cytostatic;
KW   chromosome 12p13; osteopathic; nephrotropic; antihyperphosphataemic;
KW   phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
KW   bone formation abnormality; vitamin D resistance; Paget's disease;
KW   bone calcium deficiency; kidney disorder; kidney function deficiency;
KW   renal phosphate leakage; urinary tubule acidosis; Fanconi's disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200214504-A1.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-JP06944.
XX
PR   11-AUG-2000; 2000JP-0245144.
PR   21-SEP-2000; 2000JP-0287684.
PR   22-DEC-2000; 2000JP-0391077.
PR   19-APR-2001; 2001JP-0121527.
XX
PA   (KIRI ) KIRIN BEER KK.
XX
PI   Yamashita T,  Shimada T,  Mizutani S,  Fukumoto S;
XX
DR   WPI; 2002-227350/28.
XX
PT   Polypeptides useful for regulating phosphate transport and calcium
PT   metabolism and DNA encoding them for treatment of phosphate and calcium
PT   metabolism disorders, including bone formation abnormalities and kidney
PT   diseases -
XX
PS   Claim 20; Page 172-187; 221pp; Japanese.
XX
CC   The present invention describes DNA encoding a polypeptide having the
CC   activities of inhibiting hypophosphataemia, phosphate transport and
CC   calcification, and regulating vitamin D metabolism in vivo. The
CC   polypeptide is of human origin (designated OST311) which is localised to
CC   chromosome 12p13, or is derived from this by addition, deletion and/or
CC   substitution of one or more amino acid residues. OST311 has osteopathic,
CC   nephrotropic, antihyperphosphataemic and cytostatic activities. The
CC   OST311 polypeptide regulates phosphorus transport and calcium metabolism.
CC   OST311 sequences can be used for the treatment and diagnosis of skeletal
CC   disorders such as bone cancer, bone formation abnormalities, vitamin D
CC   resistance, osteoporosis, Paget's disease and bone calcium deficiency;
CC   kidney disorders such as kidney function deficiency, renal phosphate
CC   leakage, urinary tubule acidosis and Fanconi's disease. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 13200 BP; 3710 A; 2982 C; 2903 G; 3605 T; 0 other;

  Query Match             71.4%;  Score 1151;  DB 24;  Length 13200;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-267;
  Matches 1151;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     462 CACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGAC 521
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10644 CACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGAC 10703

Qy     522 GTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTC 581
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10704 GTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTC 10763

Qy     582 CTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCC 641
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10764 CTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCC 10823

Qy     642 CTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCG 701
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10824 CTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCG 10883
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Qy     702 GAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCC 761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10884 GAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCC 10943

Qy     762 TGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGG 821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10944 TGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGG 11003

Qy     822 GTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGC 881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11004 GTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGC 11063

Qy     882 CCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCATCCCTCAGC 941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11064 CCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCATCCCTCAGC 11123

Qy     942 AAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAAAGGTGACAG 1001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11124 AAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAAAGGTGACAG 11183

Qy    1002 GGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAAC 1061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11184 GGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAAC 11243

Qy    1062 CAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCT 1121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11244 CAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCT 11303

Qy    1122 TTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGA 1181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11304 TTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGA 11363

Qy    1182 AGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCA 1241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11364 AGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCA 11423

Qy    1242 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAGTGGGTTCCTGAGCTCAAGACTTT 1301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11424 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAGTGGGTTCCTGAGCTCAAGACTTT 11483

Qy    1302 GAAGGTGTAGGGAAGAGGAAATCGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTT 1361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11484 GAAGGTGTAGGGAAGAGGAAATCGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTT 11543

Qy    1362 ATGTTAGATGCCCCGATCCCACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGA 1421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11544 ATGTTAGATGCCCCGATCCCACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGA 11603

Qy    1422 ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGG 1481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11604 ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGG 11663

Qy    1482 GGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGC 1541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11664 GGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGC 11723

Qy    1542 TTGCTGAAATGAGGCAGGAATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCT 1601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   11724 TTGCTGAAATGAGGCAGGAATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCT 11783

Qy    1602 TCTGTCTCGCT 1612
           ||||||||||||
Db   11784 TCTGTCTCGCT 11794


RESULT 8
AAC61159
ID   AAC61159 standard; cDNA; 1973 BP.
XX
AC   AAC61159;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Human fibroblast growth factor-20 (FGF-20) cDNA sequence SEQ ID 7.
XX
KW   Fibroblast growth factor-20; FGF-20; cytostatic; nootropic; metastasis;
KW   neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer;
KW   leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease;
KW   neurodegenerative disorder; Parkinson's disease; multiple sclerosis;
KW   amylotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy;
KW   Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder;
KW   haematopoietic disorder; myeloproliferative disorder; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060085-A1.
XX
PD   12-OCT-2000.
XX
PF   27-MAR-2000; 2000WO-US08076.
XX
PR   02-APR-1999;   99US-0127534.
PR   03-DEC-1999;   99US-0454470.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Curtis RAJ,  Wrighton NC;
XX
DR   WPI; 2000-647346/62.
DR   P-PSDB; AAY85639.
XX
PT   Novel nucleic acids encoding fibroblast growth factor-20, useful for
PT   detecting and modulating FGF-20 and for treating, e.g. cancer,
PT   neurodegenerative disorders, hepatic disorders and cardiovascular
PT   disorders -
XX
PS   Claim 1; Fig 10; 149pp; English.
XX
CC   Polynucleotide sequences AAC61155-C61160 encode fibroblast growth
CC   factor-20 (FGF-20) proteins AAY85637-Y85639. The invention includes
CC   FGF-20 sequences isolated from humans and monkeys. Proteins,
CC   polynucleotides, agonists and antagonists of the invention have
CC   cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant
CC   and hepatotropic activity. The peptides, nucleotides and their binding
CC   agents my be used to modulate the expression or activity of FGF-20, or to
CC   diagnose aberrant FGF-20 expression. FGF20 activity or expression may be
CC   down-regulated to treat proliferative or differentiative disorders (e.g.
CC   cancers and leukaemia), tumour angiogenesis and metastasis, skeletal
CC   dysplasia, neurodegenerative disorders (e.g. Alzheimer's disease,
CC   Parkinson's disease, multiple sclerosis, amylotrophic lateral sclerosis,
CC   progressive supranuclear palsy, epilepsy or Creutzfeldt-Jakob disease),
CC   hepatic disorders, cardiovascular disorders and haematopoietic and/or
CC   myeloproliferative disorders.
XX
SQ   Sequence 1973 BP; 580 A; 463 C; 505 G; 425 T; 0 other;

  Query Match           56.6%;  Score 912;  DB 21;  Length 1973;
  Best Local Similarity  97.4%;  Pred. No. 5e-210;
  Matches  927;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     317 GAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATC 376
           | ||||| ||| | |    |   ||       |  |    ||||||||||||||||||
Db    1022 GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATAGGTGCCCTGATGATCAGATC 1081

Qy     377 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1082 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 1141

Qy     437 TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1142 TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA 1201

Qy     497 CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1202 CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG 1261
```

```
Qy     557 TCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1262 TCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTT 1321

Qy     617 CCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCA 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1322 CCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCA 1381

Qy     677 CACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGC 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1382 CACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGC 1441

Qy     737 CCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAG 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1442 CCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAG 1501

Qy     797 CCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGG 856
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1502 CCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGG 1561

Qy     857 GGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG 916
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1562 GGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG 1621

Qy     917 CACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGAC 976
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1622 CACCCTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGAC 1681

Qy     977 GTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCC 1036
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1682 GTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCC 1741

Qy    1037 CTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGC 1096
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1742 CTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGC 1801

Qy    1097 CTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAA 1156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1802 CTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAA 1861

Qy    1157 TTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGC 1216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1862 TTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGC 1921

Qy    1217 CTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAA 1268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1922 CTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAA 1973
```

RESULT 9
AAS21376
ID AAS21376 standard; cDNA; 996 BP.
XX
AC AAS21376;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO9828 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12304.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical -
XX
PS Claim 3; Fig 265; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 996 BP; 222 A; 320 C; 260 G; 194 T; 0 other;

Query Match 49.5%; Score 798; DB 22; Length 996;
Best Local Similarity 100.0%; Pred. No. 1.2e-182;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    199 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 258

Qy    174 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCC 233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCC 318

Qy    234 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 378

Qy    294 AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATC 353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATC 438

Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 498

Qy    414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 558

Qy    474 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 618

Qy    534 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 678

Qy    594 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 738

Qy    654 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 798

Qy    714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 858

Qy    774 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 918

Qy    834 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 978

Qy    894 TTCATCTAGGGTCGCTGG 911
          ||||||||||||||||||
Db    979 TTCATCTAGGGTCGCTGG 996
```

RESULT 10
AAF44266
ID AAF44266 standard; cDNA; 996 BP.
XX
AC AAF44266;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO9828 nucleotide sequence SEQ ID NO:510.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR P-PSDB; AAB65297.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 2; Fig 323; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 996 BP; 222 A; 320 C; 260 G; 194 T; 0 other;

  Query Match   49.5%; Score 798; DB 22; Length 996;
  Best Local Similarity   100.0%; Pred. No. 1.2e-182;
  Matches 798; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 258

Qy    174 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCC 233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    259 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCC 318

Qy    234 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 378

Qy    294 AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATC 353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATC 438

Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 498

Qy    414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 558

Qy    474 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 533
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 618

Qy    534 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 593
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 678

Qy    594 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 738

Qy    654 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 798

Qy    714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 858

Qy    774 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 918

Qy    834 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 978

Qy    894 TTCATCTAGGGTCGCTGG 911
          ||||||||||||||||||
Db    979 TTCATCTAGGGTCGCTGG 996
```

RESULT 11
AAD16366
ID AAD16366 standard; DNA; 756 BP.
XX
AC AAD16366;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human sbgFGF-19b gene.
XX
KW Human; Alzheimer's disease; amyotrophic lateral sclerosis;
KW ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;
KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;
KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
KW sexual disorder; growth abnormality; infection; autoimmune disease;
KW rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
KW cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
KW diabetes mellitus; glomerulonephritis; renovascular hypertension;
KW cancer; vaccine; gene therapy; sbgFGF-19b gene; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..756
FT   /*tag= a
FT   /product= "Human sbgFGF-19b protein"
XX
PN WO200160850-A1.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US04703.
XX
PR 14-FEB-2000; 2000US-0182172.
PR 29-FEB-2000; 2000US-0186084.
PR 18-APR-2000; 2000US-0198583.
PR 04-OCT-2000; 2000US-0237963.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
DR WPI; 2001-536566/59.
DR P-PSDB; AAE09459.
XX
PT New secreted and membrane associated polypeptides for treating
PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT disorders, stroke, and asthma -
XX
PS Claim 2; Page 53-54; 94pp; English.
XX
CC The present sequence is a gene encoding human sbgFGF-19b protein,
CC a secreted protein of the invention.
CC The invention relates to secreted and membrane associated polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating diseases such as Alzheimer's disease,
CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
CC of the immune system, haematopoietic disease, inflammation, anxiety,
CC schizophrenia, feeding disorders, anorexia, depression, social, sexual
CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning
CC and memory alteration and altered immune response, seizure, migraine,
CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
CC of transsexuals, growth abnormalities, obesity, infections, autoimmune
CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
CC disorders associated with healthy maintenance of gastric mucosa and
CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
CC amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
CC viral and non-viral hepatitis, type I and type II diabetes mellitus,
CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
CC paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
CC invention are used to identify membrane bound and soluble receptors.
CC They are also useful as vaccines for inducing an immunological response
CC in a mammal. Polynucleotides of the invention are used in gene therapy.
CC They are also valuable for chromosome localisation studies and tissue
CC expression studies.
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

  Query Match   46.9%; Score 756; DB 22; Length 756;
  Best Local Similarity 100.0%; Pred. No. 1.5e-172;
  Matches 756; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120
```

```
Qy     267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy     327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy     387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||||||||||||||||||||||||||||||||||
Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
```

RESULT 12
AAH75021
ID AAH75021 standard; DNA; 756 BP.
XX
AC AAH75021;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of human fibroblast growth factor 23 (FGF-23).
XX
KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
KW congenital defect; fertility; abnormal growth; thymus function;
KW leukemia; lymphoma; autoimmune disease; proliferative disorder;
KW differentiation disorder; central nervous system disorder; infarction;
KW Parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation;
KW intestinal wound; motility disorder; absorption disorder; stroke;
KW congenital malformation; ischemic vascular disease; myocardial ischemia;
KW peripheral vascular disease; renal artery disease; bone disease;
KW musculoskeletal disease; skeletal myopathy; arthritis; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..756
FT   /*tag= a
FT   /product= "fibroblast growth factor 23 (FGF-23"
XX
PN WO200166596-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07469.
XX
PR 08-MAR-2000; 2000US-0187854.
PR 18-SEP-2000; 2000US-0233368.
PR 05-DEC-2000; 2000US-0251649.
XX
PA (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
PI Itoh N, Kavanaugh MW;
XX
DR WPI; 2001-522948/57.
DR P-PSDB; AAG63944.
XX
PT Isolated nucleic acids encoding the human and murine fibroblast growth
PT factor 23, useful in the treatment of a condition characterized by
PT inadequate function of placental cells (e.g. congenital defects) and
PT the thymus (e.g. leukemia) -
XX
PS Claim 2; Fig 3; 77pp; English.
XX
CC The present sequence encodes fibroblast growth factor 23 (FGF-23).
CC Human FGF-23 polynucleotides and polypeptides are useful for treating
CC a patient suffering from traumatic injury or a condition characterized
CC by dysfunction of or injury to skin cells, a condition characterized by
CC inadequate function of placental cells (e.g. congenital defects,
CC fertility, or abnormal growth), a condition characterized by inadequate
CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
CC proliferative disorder of the thymus, or differentiation disorder of
CC the thymus), or a condition characterized by central nervous system
CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
CC FGF-23 polynucleotide and polypeptide are also useful in the treatment
CC of Crohn's disease, healing of intestinal wounds, ulcers, inflammation,
CC injuries and surgical anastomoses, motility and absorption disorders,
CC and congenital malformations of the intestine. They are also useful for
CC treating ischemic vascular diseases (e.g. myocardial ischemia/infarction,
CC peripheral vascular disease, renal artery disease, stroke) and
CC musculoskeletal disease characterized by loss of function, inadequate
CC function or death of skeletal muscle cells, bone cells or supporting
CC cells (e.g. skeletal myopathies, bone disease, or arthritis).
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

Query Match 46.9%; Score 756; DB 22; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-172;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy     207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy     267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy     327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy     387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360
```

```
Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||||||||||||||||||||||||||||||||||
Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
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RESULT 13
AAH75033
ID AAH75033 standard; DNA; 756 BP.
XX
AC AAH75033;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of human fibroblast growth factor 23 (FGF-23).
XX
KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
KW congenital defect; fertility; thymus; leukemia; lymphoma; injury;
KW autoimmune disease; proliferative disorder; differentiation disorder;
KW central nervous system disorder; Parkinson's disease; inflammation;
KW Alzheimer's disease; Crohn's disease; intestinal wound; stroke;
KW motility disorder; absorption disorder; intestinal malformation;
KW ischemic vascular disease; myocardial ischemia; myocardial infarction;
KW peripheral vascular disease; renal artery disease; skeletal myopathy;
KW musculoskeletal disease; skeletal muscle cell; bone disease; arthritis;
KW ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..756
FT   /*tag= a
FT   /product= "fibroblast growth factor 23 (FGF-23)"
XX
PN WO200166595-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07468.
XX
PR 08-MAR-2000; 2000US-0187854.
PR 18-SEP-2000; 2000US-0233368.
PR 05-DEC-2000; 2000US-0251650.
XX
PA (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
PI Itoh N, Kavanaugh MW;
XX
DR WPI; 2001-522947/57.
DR P-PSDB; AAG63947.
XX
PT Isolated nucleic acids encoding the human and murine fibroblast growth
PT factor 23, useful in the treatment of a condition characterized by
PT inadequate function of placental cells (e.g. congenital defects) and
PT the thymus (e.g. leukemia) -
XX
PS Claim 2; Fig 3; 77pp; English.
XX
CC The present sequence encodes fibroblast growth factor 23 (FGF-23).
CC The human FGF-23 polynucleotide and polypeptide are useful for treating
CC a patient suffering from traumatic injury or a condition characterized
CC by dysfunction of or injury to skin cells, a condition characterized
CC by inadequate function of placental cells (e.g. congenital defects,
CC fertility, or abnormal growth), a condition characterized by inadequate
CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
CC proliferative disorder of the thymus, or differentiation disorder of
CC the thymus), or a condition characterized by central nervous system
CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
CC FGF-23 polynucleotide and polypeptide are also useful in the
CC treatment of Crohn's disease, healing of intestinal wounds, ulcers,
CC inflammation, injuries and surgical anastomoses, motility and
CC absorption disorders, and congenital malformations of the intestine.
CC They are also useful for treating ischemic vascular diseases (e.g.
CC myocardial ischemia/infarction, peripheral vascular disease, renal
CC artery disease, stroke) and musculoskeletal disease characterized by
CC loss of function, inadequate function or death of skeletal muscle cells,
CC bone cells or supporting cells (e.g. skeletal myopathies, bone disease,
CC or arthritis).
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

Query Match 46.9%; Score 756; DB 22; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-172;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy     207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy     267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy     327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy     387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540
```

```
Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||||||||||||||||||||||||||||||||||
Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
```

RESULT 14
ABN81575
ID ABN81575 standard; cDNA; 756 BP.
XX
AC ABN81575;
XX
DT 28-AUG-2002 (first entry)
XX
DE Human FGF23 protein encoding cDNA SEQ ID NO 1.
XX
KW Human; FGF23; haemostatic; hyperphosphataemia; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..756
FT   /*tag= a
FT   /product= "FGF23 protein"
XX
PN WO200252009-A1.
XX
PD 04-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-JP11482.
XX
PR 26-DEC-2000; 2000JP-0396316.
PR 29-MAY-2001; 2001JP-0161370.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Itoh H, Fukushima N, Saito H, Kusano K;
XX
DR WPI; 2002-508891/54.
DR P-PSDB; ABB77581.
XX
PT Human FGF23 protein mutant for lowering blood phosphorus level,
PT applicable in gene therapy remedies for hyperphosphatemia -
XX
PS Disclosure; Page 44-46; 64pp; Japanese.
XX
CC The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)
CC FGF23 and mutants FGF23 comprising an amino acid substitution of arginine
CC at position 176 to glutamine and/or position 179 to glutamine or
CC tryptophan. The mutants are generated by introducing the following base
CC changes in the nucleic acid sequence: R176Q mutant is generated by
CC G527A; R179Q is generated by G536A; and R179W is generated by C535T. The
CC protein and encoding DNA are applicable in remedies for
CC hyperphosphataemia, including gene therapy.
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

  Query Match   46.9%; Score 756; DB 24; Length 756;
  Best Local Similarity   100.0%; Pred. No. 1.5e-172;
  Matches 756; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy     207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy     267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy     327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy     387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||||||||||||||||||||||||||||||||||
Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
```

RESULT 15
ABL91738
ID ABL91738 standard; DNA; 756 BP.
XX
AC ABL91738;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 81.
XX
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX
OS Homo sapiens.
XX
PN DE10100586-C1.
XX
PD 11-APR-2002.
XX
PF 09-JAN-2001; 2001DE-1000586.

XX
PR 09-JAN-2001; 2001DE-1000586.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
DR WPI; 2002-270454/32.
XX
PT Inhibiting gene expression in cells, useful for e.g. treating tumors,
PT by introducing double-stranded complementary oligoRNA having unpaired
PT terminal bases -
XX
PS Claim 13; Page 57; 104pp; German.
XX
CC The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a
CC single-stranded segment of 1-4 nt. The method provides
CC oligoribonucleotides for antisense inhibition of gene expression useful
CC e.g. for treating tumours but the oligoribonucleotides may also be
CC directed against genes present in pathogens (e.g. Plasmodium or
CC viruses/viroids, pathogenic on humans, animals or plants) or against
CC cytokine, Id, developmental or prion genes. The method provides more
CC effective inhibition of gene expression than use of known
CC oligonucleotides, probably because the unpaired overhang increases
CC stability and thus intracellular concentration.
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

Query Match 46.9%; Score 756; DB 24; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-172;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
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Db      1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy    327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy    387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
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Qy    447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy    507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy    567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy    627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy    687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy    747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy    807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy    867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
          ||||||||||||||||||||||||||||||||||||
Db    721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
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Search completed: May 29, 2003, 00:01:36
Job time : 445 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 11:51:21 ; Search time 2480 Seconds
(without alignments)
10527.066 Million cell updates/sec

Title: US-09-901-938-1
Perfect score: 1612
Sequence: 1 cggcaaaaaggagggaatcc.....tgagcaccttctgtctcgct 1612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	571	35.4	719	17	AG095702	AG095702 Pan trogl
2	220.6	13.7	470	13	BI789859	BI789859 ic44d12.y
3	212.6	13.2	433	10	BB850709	BB850709 BB850709
4	102.8	6.4	438	17	AQ412342	AQ412342 RPCI-11-1
5	99.6	6.2	564	17	AQ570344	AQ570344 HS_5352_B
6	72.6	4.5	741	12	BE869144	BE869144 601445130
7	72.6	4.5	835	12	BE889616	BE889616 601512637
8	72.6	4.5	888	13	BI919047	BI919047 603180811
9	68.4	4.2	950	11	AK007574	AK007574 Mus muscu
10	63.8	4.0	708	12	BG328684	BG328684 602427957
c 11	56.4	3.5	925	17	CNS0091P	AL053013 Drosophil
c 12	54	3.3	1201	17	CNS016A0	AL106482 Drosophil
13	53.6	3.3	206	10	AW395897	AW395897 sh07b05.y
c 14	53.4	3.3	889	17	CNS006MT	AL065765 Drosophil
c 15	52.4	3.3	796	17	CNS0118D	AL099943 Drosophil
c 16	52	3.2	1024	12	BE965125	BE965125 601658918
17	51.8	3.2	152	12	BE877210	BE877210 601485130
c 18	51.8	3.2	421	9	AI961371	AI961371 wt17f04.x
19	51.8	3.2	530	12	BG308044	BG308044 fm56b06.y
20	51.8	3.2	839	17	CNS004NB	AL054280 Drosophil
c 21	51.6	3.2	215	9	AI874303	AI874303 wm50h10.x
22	51.4	3.2	594	10	BB619211	BB619211 BB619211
23	51.4	3.2	600	12	BG807855	BG807855 2072-92 M
c 24	51.4	3.2	1017	17	CNS015K4	AL105550 Drosophil
c 25	51.2	3.2	820	12	BE964506	BE964506 601658618
26	51.2	3.2	921	12	BG282532	BG282532 602406405
c 27	50.8	3.2	634	9	AL514497	AL514497 AL514497
c 28	50.8	3.2	1076	17	CNS015ZO	AL106110 Drosophil
c 29	50.6	3.1	1124	17	CNS073BM	AL427304 clone BA0
30	50.4	3.1	316	13	BI506901	BI506901 BB170029A
c 31	50.4	3.1	319	9	AA814555	AA814555 of42f07.s
32	50.4	3.1	339	9	AI590021	AI590021 tr74h11.x
33	50.4	3.1	653	12	BG170925	BG170925 602323695
c 34	50.4	3.1	671	9	AL514097	AL514097 AL514097
35	50.2	3.1	119	12	BG670429	BG670429 DRNBBB03
c 36	50.2	3.1	153	12	BE874163	BE874163 601484347
37	50.2	3.1	544	14	C93698	C93698 C93698 Dict
c 38	50	3.1	368	9	AA828436	AA828436 oc46c05.s
c 39	50	3.1	440	9	AI359279	AI359279 qy27d12.x
c 40	50	3.1	468	9	AL514541	AL514541 AL514541
c 41	50	3.1	1884	12	BF530637	BF530637 602071926
42	49.8	3.1	1201	17	CNS016B1	AL106519 Drosophil
43	49.6	3.1	322	9	AA213024	AA213024 mw86h08.r
44	49.6	3.1	399	12	BG384192	BG384192 303172 MA
c 45	49.4	3.1	404	9	AI860694	AI860694 wl15b12.x

ALIGNMENTS

RESULT 1
AG095702
LOCUS AG095702 719 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-096N15.R, genomic survey sequence.
ACCESSION AG095702
VERSION AG095702.1 GI:16647544
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-096N15.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 719)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

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            PRIMERS
                Sequencing: M13Rev
            LIBRARY
                Vector    : pKS145
                R.Site 1  : SacI
                R.Site 2  : SacI.
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                    /clone="PTB-096N15.R"
                    /sex="male"
                    /cell_type="lymphoblast"
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BASE COUNT      171 a    194 c    175 g    177 t      2 others
ORIGIN

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  Best Local Similarity  93.0%;  Pred. No. 3.5e-89;
  Matches  613;  Conservative    0;  Mismatches   35;  Indels   11;  Gaps    1;

Qy     749 GGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAG 808
           || ||    ||    | | |  ||||||||||||||||||||||||||||||||||||||
Db      70 GGGCCGCCGCTAGCATGCTCGAGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAG 129

Qy     809 TGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCC 868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 TGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCC 189

Qy     869 GGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAA 928
           ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     190 GGAAGGCTGCCGCCCCTTCCCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAA 249

Qy     929 CCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATG 988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 CCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATG 309

Qy     989 GGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAG 1048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 GGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAG 369

Qy    1049 GTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCC 1108
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 GTCCTGTGAGAATCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCC 429

Qy    1109 ATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCAT 1168
           |||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Db     430 ATATAGAACACCTTTCCGAATAGGAAACCCCAACAGGTAAACTAGAAATTTTCCCTTCAT 489

Qy    1169 GAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTA 1228
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Db     490 GAAGGTAGAGAGAAGGGGTCTATCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTA 549

Qy    1229 TCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAGTGGGTTCCTG 1288
           |||||||||||||| |||||||||||||||||| |           || ||||||
Db     550 TCACTTTTAAGCATATAAAAAAAAAAAAAAAAAAAACA----------GTGGGTTTCCTG 598

Qy    1289 AGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCAGAAGCTTCTCCACT 1348
           || |||| |||||||  |||||||||||||||| ||||||||||||||||||  |||||
Db     599 AGTTCAACACTTTGACAGTGTAGGGAAGAGGAGATCGGAGATCCCAGAAGCTTTCCCACT 658

Qy    1349 GCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAGTGTGCAAACCTTG 1407
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Db     659 GCCCTATGCATTTATGTCAGATGCCCCGATCCCACTGCCCTTCGAGTGTGCAAACCTTG 717


RESULT 2
BI789859
LOCUS       BI789859                470 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  ic44d12.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
            musculus cDNA clone IMAGE:5656391 5', mRNA sequence.
ACCESSION   BI789859
VERSION     BI789859.1  GI:15817584
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Douglas Melton DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Juliana Brown
            (brown@fas.harvard.edu)
            MGI:1942717 This sequence now available from the IMAGE consortium,
            for clone orders contact: info@image.llnl.gov
            Seq primer: -40RP from Gibco
            High quality sequence stop: 458.
FEATURES            Location/Qualifiers
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                    adult islet"
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                    adult, mixed"
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                    /note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five
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                    pancreas,  newborn pancreas, adult pancreas, and adult
                    islets of Langerhans were  seperately constructed using
                    SuperScript Plasmid Library kit (Life  Technologies). cDNA
                    was made by oligo-dT priming and size-selected by  column
                    fractionation. Libraries were amplified once on solid
                    support  and plasmid DNA from each library was prepared
                    and mixed in equal  amounts. The mixed library DNA was
                    normalized by method #4 from  Bonaldo, Lennon, and Soares
                    1996 Genome Research 6:791-806; 0.5  microgram
                    single-stranded mixed library plasmid DNA was mixed with
                    5 micrograms PCR product representing mixed library
                    inserts and  hybridized to an Ecot of 6. Single-stranded
                    (unhybridized) plasmids  were isolated by hydroxyapatite
                    chromatography and used to make this  library."
BASE COUNT       75 a    166 c    139 g     89 t      1 others
ORIGIN

  Query Match           13.7%;  Score 220.6;  DB 13;  Length 470;
  Best Local Similarity  69.0%;  Pred. No. 1.5e-28;
  Matches  301;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy     466 ATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCT 525
           | |||  ||| ||||| |||| |||||  ||   ||||||||| || |  || |||||||
Db      35 ACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTGGAGAATGTCTATGACGTCT 94

Qy     526 ACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGC 585
           ||   || |   || |||||| |||||| || |||||||| || ||| |   |||||  ||
Db      95 ACTTGTCGCAGAAGCATCACTACCTGGTGAGCCTGGGCCGCGCCAAGCGCATCTTCCAGC 154
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Qy    586 CAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAA 645
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Qy    646 TTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGC 705
Db    215 TGTTCTTCNACACTGTTCGCCCACGGCGCCACACGCGCAGCGCCGAGGACCCACCCGAGC 274

Qy    706 GGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTT 765
Db    275 GCGACCCACTGAACGTGCTCAAGCCGCGGCCCCGCGCCACGCCTGTGCCTGTATCCTGCT 334

Qy    766 CACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGG 825
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Qy    826 TCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCT 885
Db    395 TGCGCAGAGGCCGTGGAGATGCTCGCGGGGGCGCGGGAGGCGCGGATAGGTGTCGCCCCT 454

Qy    886 TCGCCAAGTTCATCTA 901
Db    455 TTCCCAGGTTCGTCTA 470
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RESULT 3
BB850709
LOCUS BB850709 433 bp mRNA linear EST 26-NOV-2001
DEFINITION BB850709 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930108M15 5', mRNA sequence.
ACCESSION BB850709
VERSION BB850709.1 GI:17092163
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 433)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
FEATURES Location/Qualifiers
source 1. .433
/organism="Mus musculus"
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/tissue_type="inner ear"
/dev_stage="adult"
/note="pooled tissues ; (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"
BASE COUNT 102 a 128 c 108 g 95 t
ORIGIN

Query Match 13.2%; Score 212.6; DB 10; Length 433;
Best Local Similarity 74.6%; Pred. No. 3.6e-27;
Matches 311; Conservative 0; Mismatches 94; Indels 12; Gaps 3;

```
Qy     39 CAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTCCCGACA 98
Db     28 CAGCTTCTTCCTAGGAAGAAGAGAAAGGCCAGCAAGGGCCCAGCCTG---------TCTG 78

Qy     99 GGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCC 158
Db     79 GGAGTGTCAGATATCAAACTCAGAATTAGCCACTCAGTGATGTGCA--ATGCTAGGGACC 136

Qy    159 CGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCC 218
Db    137 TGCCTTAGACTCCTGGTGGGCGTGCTCTGCACTGTCTGCAGCTTGGGCACTGCTAGAGCC 196

Qy    219 TATCCCAATGCCTCCCCACTGCTCGGCTCC-AGCTGGGGTGGCCTGATCCACCTGTACAC 277
Db    197 TATCCAGACACTTCCCCATTGCTTGGCTCCAACCTGGGGAAGCCTGACCCACCTGTACAC 256

Qy    278 AGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGC 337
Db    257 GGCTACAGCCAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCATGTAGATGGCAC 316

Qy    338 ACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGT 397
Db    317 CCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACGCCGGCTCTGTGGT 376

Qy    398 GATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTT 454
Db    377 GATAACAGGAGCCATGACTCGAAGGTTCCTTTGTATGGATCTCCACGGCAACATTTT 433
```

RESULT 4
AQ412342
LOCUS AQ412342 438 bp DNA linear GSS 23-MAR-1999
DEFINITION RPCI-11-177D20.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-177D20, DNA sequence.
ACCESSION AQ412342
VERSION AQ412342.1 GI:4471830
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 438)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

```
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-177D20.TV
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .438
                      /organism="Homo sapiens"
                      /db_xref="GDB:7567675"
                      /db_xref="taxon:9606"
                      /clone="RPCI-11-177D20"
                      /clone_lib="RPCI-11"
                      /sex="Male"
                      /cell_type="Lymphocytes"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      RPCI11 Human Male BAC Library"
BASE COUNT      123 a     73 c    116 g    126 t
ORIGIN

  Query Match             6.4%;  Score 102.8;  DB 17;  Length 438;
  Best Local Similarity   79.2%;  Pred. No. 3.4e-08;
  Matches  122;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy     317 GAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATC 376
           | ||||| ||| |  |    |   ||        | |    ||||||||||||||||||
Db     213 GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATATGTGCCCTGATGATCAGATC 272

Qy     377 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     273 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 332

Qy     437 TTTCAGAGGCAACATTTTTGGATCACACTATTTC 470
           ||||||| ||||||| |||||||||     ||||
Db     333 TTTCAGATGCAACATATTTGGATCATTGAGTTTC 366


RESULT 5
AQ570344
LOCUS       AQ570344                564 bp    DNA     linear   GSS 01-JUN-1999
DEFINITION  HS_5352_B1_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=928 Col=17 Row=N, DNA sequence.
ACCESSION   AQ570344
VERSION     AQ570344.1  GI:4963564
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 928  row: N  column: 17
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 564.
FEATURES              Location/Qualifiers
     source           1. .564
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="Plate=928 Col=17 Row=N"
                      /clone_lib="RPCI-11 Human Male BAC Library"
                      /sex="male"
                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                      Male blood DNA was isolated from one randomly chosen donor
                      and partially digested with a combination of EcoRI and
                      EcoRI Methylase. Size selected DNA was cloned into the
                      pBACe3.6 vector at EcoRI sites"
BASE COUNT      152 a    100 c    138 g    169 t      5 others
ORIGIN

  Query Match             6.2%;  Score 99.6;  DB 17;  Length 564;
  Best Local Similarity   77.9%;  Pred. No. 1.1e-07;
  Matches  120;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy     317 GAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATC 376
           | ||||| ||| |  |    |   ||        | |    ||||||||||||||||||
Db     244 GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATAGGTGCCCTGATGATCAGATC 303

Qy     377 AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 436
           | ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     304 ACAGGATGCTGGCTTTGTGGTGATTACACGTGTGATGAGCAGAAGATACCTCTGCATGGA 363

Qy     437 TTTCAGAGGCAACATTTTTGGATCACACTATTTC 470
           ||||||| ||||||||| |||||||     ||||
Db     364 TTTCAGATGCAACATTTGTGGATCAGTGAGTTTC 397


RESULT 6
BE869144
LOCUS       BE869144                741 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601445130F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849343 5',
            mRNA sequence.
ACCESSION   BE869144
VERSION     BE869144.1  GI:10317920
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9566  row: k  column: 08
            High quality sequence stop: 696.
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FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3849343"
                     /clone_lib="NIH_MGC_65"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "
BASE COUNT      122 a    259 c    235 g    125 t
ORIGIN

  Query Match             4.5%;  Score 72.6;  DB 12;  Length 741;
  Best Local Similarity   53.8%;  Pred. No. 0.0048;
  Matches  150;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy     293 CAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCAT 352
           ||||| |  |||||  ||||       | |||   |||||  |||| |      |||| |
Db     277 CAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGCCAGAGCGC 336

Qy     353 CTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGAT 412
           |||||   |||  |||||   |||  | |    |    ||||  || |  || |||
Db     337 GCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGCA 396

Qy     413 GAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGA 472
           |||    | |||||||||||||    |   ||||| ||    ||    |   | | |
Db     397 CAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTC 456

Qy     473 CCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
           |||  ||||    ||| |  | ||| |    | | || ||| | || ||||  ||
Db     457 GGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATC 516

Qy     533 TCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAA 571
           || | | | ||| ||||   ||| || | || ||
Db     517 CGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAA 555


RESULT 7
BE889616
LOCUS       BE889616                 835 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601512637F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914192 5',
            mRNA sequence.
ACCESSION   BE889616
VERSION     BE889616.1  GI:10347118
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9735  row: i  column: 09
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3914192"
                     /clone_lib="NIH_MGC_71"
                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
BASE COUNT      139 a    284 c    267 g    145 t
ORIGIN

  Query Match             4.5%;  Score 72.6;  DB 12;  Length 835;
  Best Local Similarity   53.8%;  Pred. No. 0.0046;
  Matches  150;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy     293 CAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCAT 352
           ||||| |  |||||  ||||       | |||   |||||  |||| |      |||| |
Db     285 CAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGCCAGAGCGC 344

Qy     353 CTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGAT 412
           |||||   |||  |||||   |||  | |    |    ||||  || |  || |||
Db     345 GCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGCA 404

Qy     413 GAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGA 472
           |||    | |||||||||||||    |   ||||| ||    ||    |   | | |
Db     405 CAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTC 464

Qy     473 CCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
           |||  ||||    ||| |  | ||| |    | | || ||| | || ||||  ||
Db     465 GGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATC 524

Qy     533 TCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAA 571
           || | | | ||| ||||   ||| || | || ||
Db     525 CGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAA 563


RESULT 8
BI919047
LOCUS       BI919047                 888 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  603180811F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245034 5',
            mRNA sequence.
ACCESSION   BI919047
VERSION     BI919047.1  GI:16200101
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11618  row: e  column: 03
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1. .888
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5245034"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
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0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
BASE COUNT 150 a 305 c 282 g 151 t
ORIGIN

Query Match 4.5%; Score 72.6; DB 13; Length 888;
Best Local Similarity 53.8%; Pred. No. 0.0045;
Matches 150; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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Qy    293 CAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCAT 352
          ||||| | ||||| |||| | ||| ||||| |||| |  |||| |
Db    396 CAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGCCAGAGCGC 455

Qy    353 CTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGAT 412
           |||||  ||| |||||  ||| | |  |  ||||  || |  || |||
Db    456 GCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGCA 515

Qy    413 GAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGA 472
           |||   | ||||||||||||||   |  ||||| ||   ||   |  | | |
Db    516 CAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTC 575

Qy    473 CCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
             |||  ||||   ||| |  |  ||| |    | | || ||| | || ||||  ||
Db    576 GGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATC 635

Qy    533 TCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAA 571
            || | | || || ||||  ||| || | || ||
Db    636 CGAGAAGCACCGCTCCCCGGTCTCCCTGAGCAGTGCCAA 674
```

RESULT 9
AK007574
LOCUS AK007574 950 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810021F21:fibroblast growth factor 21, full insert sequence.
ACCESSION AK007574
VERSION AK007574.1 GI:12841202
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 10 day old male pancreas cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1810021F21.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5 (bases 1 to 950)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.
FEATURES Location/Qualifiers
source 1. .950
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:1810021F21"
/db_xref="MGD:MGI:1901172"
/db_xref="taxon:10090"
/clone="1810021F21"
/sex="male"
/tissue_type="pancreas"

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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 day old"
     gene            1. .950
                     /gene="Fgf21"
     CDS             185. .817
                     /gene="Fgf21"
                     /note="data source:MGD, source key:MGI:1861377,
                     evidence:ISS
                     fibroblast growth factor 21
                     putative"
                     /codon_start=1
                     /protein_id="BAB25115.1"
                     /db_xref="GI:12841203"
                     /db_xref="MGD:MGI:1861377"
                     /translation="MEWMRSRVGTLGLWVRLLLAVFLLGVYQAYPIPDSSPLLQFGGQ
                     VRQRYLYTDDDQDTEAHLEIREDGTVVGAAHRSPESLLELKALKPGVIQILGVKASRF
                     LCQQPDGALYGSPHFDPEACSFRELLLEDGYNVYQSEAHGLPLRLPQKDSPNQDATSW
                     GPVRFLPMPGLLHEPQDQAGFLPPEPPDVGSSDPLSMVEPLQGRSPSYAS"
BASE COUNT       204 a    278 c    241 g    227 t
ORIGIN

  Query Match             4.2%;  Score 68.4;  DB 11;  Length 950;
  Best Local Similarity   53.8%;  Pred. No. 0.024;
  Matches  141;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;

Qy     299 CCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAG 358
           ||||||| |||||     || ||||    ||||  |||||| | || |   |      | ||
Db     364 CCACCTGGAGATCAGGGAGGATGGAACAGTGGTAGGCGCAGCACACCGCAGTCCAGAAAG 423

Qy     359 TGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAG 418
           |  ||||  | ||| | |    | |  | ||  |   |     ||     ||||| |     |
Db     424 TCTCCTGGAGCTCAAAGCCTTGAAGCCAGGGGTCATTCAAATCCTGGGTGTCAAAGCCTC 483

Qy     419 AAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGA 478
           || |  || |||     |         ||      | | |||||| |    | || || || ||
Db     484 TAGGTTTCTTTGCCAACAGCCAGATGGAGCTCTCTATGGATCGCCTCACTTTGATCCTGA 543

Qy     479 GAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCA 538
           |  |||||| |||  | | | |. ||||||  |||| ||| | || ||||| |||
Db     544 GGCCTGCAGCTTCAGAGAACTGCTGCTGGAGGACGGTTACAATGTGTACCAGTCTGAAGC 603

Qy     539 GTATCACTTCCTGGTCAGTCTG 560
           ||  | | |   |  |||||
Db     604 CCATGGCCTGCCCCTGCGTCTG 625


RESULT 10
BG328684
LOCUS       BG328684                 708 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602427957F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4547223 5',
            mRNA sequence.
ACCESSION   BG328684
VERSION     BG328684.1  GI:13135122
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1235  row: a  column: 16
            High quality sequence stop: 708.
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4547223"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT       115 a    247 c    227 g    119 t
ORIGIN

  Query Match             4.0%;  Score 63.8;  DB 12;  Length 708;
  Best Local Similarity   52.9%;  Pred. No. 0.16;
  Matches  137;  Conservative    0;  Mismatches  122;  Indels    0;  Gaps    0;

Qy     293 CAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCAT 352
           |||||  |  |||||  ||||       | |||   |||||  ||||  |      |||| |
Db     305 CAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGCCAGAGCGC 364

Qy     353 CTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGAT 412
           |||||   |||  |||||   |||  | |     |    ||||  || |  || |||
Db     365 GCACAGTTGGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGCA 424

Qy     413 GAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGA 472
           |||    | ||||||||||||||    |  |||||  ||    ||    |  | | |
Db     425 CAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTC 484

Qy     473 CCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
           |||  ||||     ||| |  |  |||  |    | | || ||| | || ||||  ||
Db     485 GGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATC 544

Qy     533 TCCTCAGTATCACTTCCTG 551
           || | | || || |
Db     545 CGAGAAGCACCGCTCCCGG 563


RESULT 11
CNS0091P/c
LOCUS       CNS0091P                 925 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL053013
VERSION     AL053013.1  GI:4934461
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 925)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
```

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```
FEATURES             Location/Qualifiers
     source          1. .925
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR19D16"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT      120 a     61 c     61 g    172 t    511 others
ORIGIN

  Query Match             3.5%;  Score 56.4;  DB 17;  Length 925;
  Best Local Similarity   15.5%;  Pred. No. 2.8;
  Matches   57;  Conservative  157;  Mismatches  153;  Indels    0;  Gaps    0;

Qy     560 GGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCT 619
           ::::: ::::  : : ::   :: :   : |:: |::: || || |: |: :  :|
Db     888 BSSSSTSSMSSSSBSSSSGSSSSSSGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCC 829

Qy     620 GTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACAC 679
           |  : :|:::|:|    :    :  |  :::  :| : ::::|   |   :::::  :
Db     828 GSASARGVKVRASGGAGKRGGGSGGASASHSSSSACBSSSSSCSASCWSASSSSSASSSR 769

Qy     680 CCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCG 739
           : :| | | :||::  : : :::|: |::::: :: :  |: ::    : :::: :::::
Db     768 SRSGGGAGGSGASSSRSSSSSSSASAGSVVSSASSSSSSCSSSVSCSSVASSMSCSSBSS 709

Qy     740 GATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCC 799
           :  :|::::::::: :  :| ||   :: : :   : :  : ::::::  : : ::|:::
Db     708 SSASASSSSSSSSASCASCSCCCTSWSCSCSTSASMSAARSSSSSSSSCSSSSMSASSSA 649

Qy     800 GATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGG 859
           :  : :: : : :::       |:  :   |:|::::  :|:: :: :  |  :|: ||||:
Db     648 SSSSASSSSSSGSSSSSGSACGBSMSSGGGSGSVSASSGMSSSVSSSGGRSSGSGGGGGV 589

Qy     860 AACGGGCCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCAC 919
             :|:::: :|  ||: ::|:|::   |:|:  :   |    :   ||:  |  ::||
Db     588 GGSGSSSSGSGSSGGSGSVCSCSSGCMCRCSCSSAAAAAASCVAASCGMMCGKSKSGCTN 529

Qy     920 CCTCTTT 926
             | |
Db     528 NNNNTNT 522
```

```
RESULT 12
CNS016A0/c
LOCUS       CNS016A0                1201 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN15A08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106482
VERSION     AL106482.1  GI:5622169
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACN15A08"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
BASE COUNT      411 a    141 c     84 g    322 t    243 others
ORIGIN

  Query Match             3.3%;  Score 54;  DB 17;  Length 1201;
  Best Local Similarity   46.6%;  Pred. No. 6.8;
  Matches   81;  Conservative   23;  Mismatches   70;  Indels    0;  Gaps    0;

Qy    1101 CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC 1160
           ||| |::|:|||        ::|    || |  |||    |: ||  | | :| | :|||
Db     603 CTCYCYYCHTATTTTYTTTMYTCTWAAAAAAAAAAATATADAAGAGAGAAWAWATWTTTK 544

Qy    1161 CCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCT 1220
           :::| :|    ||:|:| ::    ||| |    :  | ::|  :  : || |   | :
Db     543 KGMYYCGHGTTTATAKASACWMTATHTCTATATATWTTTTWYTACMCCYTTTTTTTTTTY 484

Qy    1221 CCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
           |  | |||| | |||      |||||||||| ||||:|||||||||||||||||
Db     483 RCMATATATCTCCTTTTTNNNAAAAAAAAAAANAAAARAAAAAAAAAAAAAAAA 430
```

```
RESULT 13
AW395897
LOCUS       AW395897                206 bp    mRNA    linear   EST 03-DEC-2001
DEFINITION  sh07b05.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1016-4042 5', mRNA sequence.
ACCESSION   AW395897
VERSION     AW395897.1  GI:6914367
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 206)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 136.
FEATURES             Location/Qualifiers
     source          1. .206
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-4042"
                     /clone_lib="Gm-c1016"
```

/tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
BASE COUNT 134 a 17 c 17 g 38 t
ORIGIN

Query Match 3.3%; Score 53.6; DB 10; Length 206;
Best Local Similarity 66.4%; Pred. No. 14;
Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
Qy   1159 TCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCT 1218
          | | | |  |||| | |  | || ||||    |    ||  ||  |||| |  |  |
Db     19 TTCGCCTATTGAAATTTGCTAAAAAGGGTTCAACAGGTAATTGTTTACTTCTTGATATCA 78

Qy   1219 CTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
            |||| || |||||||| |  | ||||||||||||||||||||||||||||||||||
Db     79 AGCCTCATTTTCACTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 134
```

RESULT 14
CNS006MT/c
LOCUS CNS006MT 889 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14K09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065765
VERSION AL065765.1 GI:4944645
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 889)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .889
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR14K09"
/clone_lib="RPCI-98"
/note="end : TET3"
BASE COUNT 307 a 36 c 68 g 252 t 226 others
ORIGIN

Query Match 3.3%; Score 53.4; DB 17; Length 889;
Best Local Similarity 44.9%; Pred. No. 9.5;
Matches 89; Conservative 24; Mismatches 85; Indels 0; Gaps 0;

```
Qy   1077 AAGTCATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAAC 1136
          ||||  :|    ||   |::  || :|| |: : | |:|    : |:||| |   |      |
Db    478 AAGTTWTWAYTTTCTTCYDTWTTTYTCTCYTMAAAWATTTHSCYTTTTCTCTTTACYYTC 419

Qy   1137 CCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAA 1196
            |   :  |||: |   : | ||| |:   | ||   | |   ||    | |:|  ::|
Db    418 AACYYTWWTTAAWTTTWTMTTCTCCTCYATCTAAAAAAAAATTCAATATTTTTMTTAMWA 359

Qy   1197 CATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAA 1256
            |   | | | | || | :::: : :  : |: || |  ||  | || ||||||||||
Db    358 TTTTAATTTTTACTTTCTHYYYMAMTWAAYAAWAACATAAAAANAAAANAAAAAAAAAAA 299

Qy   1257 AAAAAAAAAAAAAAAAAA 1274
          | ||||||||||||||||
Db    298 ANAAAAAAAAAAAAAAAA 281
```

RESULT 15
CNS0118D/c
LOCUS CNS0118D 796 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN05J08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL099943
VERSION AL099943.1 GI:5611554
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 796)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .796
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN05J08"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
BASE COUNT 33 a 20 c 70 g 537 t 136 others
ORIGIN

Query Match 3.3%; Score 52.4; DB 17; Length 796;
Best Local Similarity 29.6%; Pred. No. 15;
Matches 58; Conservative 66; Mismatches 72; Indels 0; Gaps 0;

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Db    701 SBCCCKGTCKSCCCCCCYTCTCMCCCCYCCMKCRCKYYMTGKKTHMKMYMBMKKMMKMCK 642

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Qy   1259 AAAAAAAAAAAAAAAA 1274
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Search completed: May 28, 2003, 14:14:08
Job time : 2498 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 256 Seconds
(without alignments)
8314.786 Million cell updates/sec

Title: US-09-901-938-1
Perfect score: 1612
Sequence: 1 cggcaaaaaggagggaatcc.....tgagcaccttctgtctcgct 1612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1612	100.0	1612	9	US-09-901-938-1	Sequence 1, Appli
2	1238.4	76.8	1240	10	US-09-731-872-57	Sequence 57, Appl
3	1237.4	76.8	1239	9	US-09-924-340-25	Sequence 25, Appl
4	1237.4	76.8	1239	9	US-09-992-600A-25	Sequence 25, Appl
5	1237.4	76.8	1239	9	US-10-000-489-25	Sequence 25, Appl
6	1211	75.1	1211	10	US-09-754-634A-1	Sequence 1, Appli
7	798	49.5	996	9	US-09-992-598-510	Sequence 510, App
8	798	49.5	996	9	US-09-989-293A-510	Sequence 510, App
9	798	49.5	996	9	US-09-989-735-510	Sequence 510, App
10	798	49.5	996	9	US-09-990-444-510	Sequence 510, App
11	798	49.5	996	9	US-09-989-730-510	Sequence 510, App
12	798	49.5	996	9	US-09-990-436-510	Sequence 510, App
13	798	49.5	996	9	US-09-991-181-510	Sequence 510, App
14	798	49.5	996	9	US-09-993-687-510	Sequence 510, App
15	798	49.5	996	9	US-09-989-734-510	Sequence 510, App
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18	798	49.5	996	9	US-09-993-667-510	Sequence 510, App
19	798	49.5	996	9	US-10-121-049-265	Sequence 265, App
20	798	49.5	996	9	US-10-123-904-265	Sequence 265, App
21	798	49.5	996	9	US-10-140-470-265	Sequence 265, App
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23	798	49.5	996	9	US-09-990-562-510	Sequence 510, App
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43	798	49.5	996	9	US-10-123-262-265	Sequence 265, App
44	798	49.5	996	9	US-10-142-423-265	Sequence 265, App
45	798	49.5	996	9	US-09-990-443-510	Sequence 510, App

ALIGNMENTS

RESULT 1
US-09-901-938-1
; Sequence 1, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-901-938-1

Query Match 100.0%; Score 1612; DB 9; Length 1612;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 CGGCAAAAAGGAGGGAATCCAGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGG 60

Qy      61 AAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCA 120
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Db     121 GCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTG 180

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Db     181 CCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGC 240
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RESULT 2
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; Sequence 57, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 57
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..879
; NAME/KEY: sig_peptide
; LOCATION: 127..198
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.38660866264012
; OTHER INFORMATION: seq ALCSVCSMSVLRA/YP
US-09-731-872-57

Query Match 76.8%; Score 1238.4; DB 10; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    741 ATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCG 800
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Db    781 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 840

Qy    861 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 920
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Qy    921 CTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC 980
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Db    901 CTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC 960

Qy    981 CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTC 1040
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Db    961 CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTC 1020

Qy   1041 CACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTC 1100
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Qy   1101 CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC 1160
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Qy   1161 CCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCT 1220
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Qy   1221 CCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAA 1260
          |||||||||||||||||||| ||||||||||||||||||
Db   1201 CCTCTTTATCACTTTTAAGCATGAAAAAAAAAAAAAAAAA 1240

RESULT 3
US-09-924-340-25
; Sequence 25, Application US/09924340
; Publication No. US20030027248A1
;
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/924,340
;  CURRENT FILING DATE:  2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 25
;   LENGTH: 1239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..126
;   NAME/KEY: CDS
;   LOCATION: 127..879
;   NAME/KEY: 3'UTR
;   LOCATION: 880..1239
;   NAME/KEY: polyA_site
;   LOCATION: 1224..1239
US-09-924-340-25

  Query Match             76.8%;  Score 1237.4;  DB 9;  Length 1239;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1238;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     21 AGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGG 80
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Qy     81 GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG 140
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Db     61 GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG 120

Qy    141 GGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC 200
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Db    121 GGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC 180

Qy    201 ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC 260
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Db    181 ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC 240

Qy    261 CTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAAT 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    321 GGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAG 380
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Qy    381 GATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTC 440
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Qy    441 AGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAG 500
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Qy    501 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 560
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Db    481 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 540

Qy    561 GGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTG 620
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Db       601 TCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACC 660

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Qy       861 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 920
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Db       841 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 900

Qy       921 CTCTTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC 980
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RESULT 4
US-09-992-600A-25
; Sequence 25, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT: Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US4.DIV
;  CURRENT APPLICATION NUMBER: US/09/992,600A
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: JPatent
; SEQ ID NO 25
;   LENGTH: 1239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..126
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 127..879
;   FEATURE:
;   NAME/KEY: 3'UTR
;   LOCATION: 880..1239
;   FEATURE:
;   NAME/KEY: polyA_site
;   LOCATION: 1224..1239
US-09-992-600A-25

  Query Match             76.8%;  Score 1237.4;  DB 9;  Length 1239;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1238;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        21 AGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGG 80
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Qy        81 GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG 140
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Qy       201 ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC 260
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Qy       261 CTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAAT 320
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Qy       381 GATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTC 440
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Db       421 AGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAG 480

Qy       501 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 560
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Db       481 ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG 540

Qy       561 GGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTG 620
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Qy       681 CGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGG 740
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Qy     801 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 860
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Db     781 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 840

Qy     861 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1041 CACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTC 1100
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Qy    1101 CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC 1160
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Db    1201 CCTCTTTATCACTTTTAAGCATGAAAAAAAAAAAAAAAA 1239
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RESULT 5
US-10-000-489-25
; Sequence 25, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 25
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..126
; NAME/KEY: CDS
; LOCATION: 127..879
; NAME/KEY: 3'UTR
; LOCATION: 880..1239
; NAME/KEY: polyA_site
; LOCATION: 1224..1239
US-10-000-489-25

Query Match 76.8%; Score 1237.4; DB 9; Length 1239;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      21 AGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGG 80
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Db     661 CGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGG 720

Qy     741 ATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCG 800
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Db     781 ATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGA 840

Qy     861 ACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACC 920
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RESULT 6
US-09-754-634A-1
; Sequence 1, Application US/09754634A
; Patent No. US20010044525A1
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell C.
;  TITLE OF INVENTION: FGF HOMOLOG ZFGF12
;  FILE REFERENCE: 00-02
;  CURRENT APPLICATION NUMBER: US/09/754,634A
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/174,582
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1211
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (115)...(870)
US-09-754-634A-1

  Query Match             75.1%;  Score 1211;  DB 10;  Length 1211;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1211;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 92
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Db       1 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 60

Qy      93 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 152
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Db      61 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 120

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Qy     273 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 332
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Qy     573 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 632
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Db     661 GACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCC 720

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Qy     873 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 932
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Qy    1113 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1172
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Qy    1233 TTTTAAGCATA 1243
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Db    1201 TTTTAAGCATA 1211


RESULT 7
US-09-992-598-510
; Sequence 510, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
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Qy    414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
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Db    679 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 738

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RESULT 8
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; Sequence 510, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
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Qy    594 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 653
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Db    979 TTCATCTAGGGTCGCTGG 996
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RESULT 9
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; Sequence 510, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 510, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C19
;  CURRENT APPLICATION NUMBER: US/09/990,444
;  CURRENT FILING DATE:  2001-11-14
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;  PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 173
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Db    259 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCC 318

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Db    319 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 378

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Db    379 AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATC 438

Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
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Db    439 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 498

Qy    414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
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Db    499 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 558

Qy    474 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 533
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Db    619 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 678

Qy    594 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 653
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Db    679 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 738

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Db     979 TTCATCTAGGGTCGCTGG 996
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RESULT 11
US-09-989-730-510
; Sequence 510, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    234 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 293
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Db    439 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 498

Qy    414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
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Db    559 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 618

Qy    534 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 593
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Db    619 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 678

Qy    594 AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC 653
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Qy    654 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 713
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Db    739 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 798

Qy    714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 773
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Qy    834 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 893
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RESULT 12
US-09-990-436-510
; Sequence 510, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone

; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    199 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 258

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Qy    354 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 413
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Qy    474 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 533
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Qy    894 TTCATCTAGGGTCGCTGG 911
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Db    979 TTCATCTAGGGTCGCTGG 996
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RESULT 13
US-09-991-181-510
; Sequence 510, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             49.5%;  Score 798;  DB 9;  Length 996;
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Db     439 TACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATG 498

Qy     414 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 473
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Db     499 AGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGAC 558

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Db     559 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCT 618

Qy     534 CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATG 593
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Db     739 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 798

Qy     714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 773
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Qy     834 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 893
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Qy     894 TTCATCTAGGGTCGCTGG 911
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Db     979 TTCATCTAGGGTCGCTGG 996


RESULT 14
US-09-993-687-510
; Sequence 510, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C11
;  CURRENT APPLICATION NUMBER: US/09/993,687
;  CURRENT FILING DATE:  2002-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 510, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
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; APPLICANT: Roy,Margaret Ann
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Williams,P. Mickey
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 49.5%; Score 798; DB 9; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.3e-216;
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    739 AACACCCCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCC 798

Qy    714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG 858

Qy    774 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC 918

Qy    834 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    894 TTCATCTAGGGTCGCTGG 911
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Db    979 TTCATCTAGGGTCGCTGG 996
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Search completed: May 29, 2003, 00:05:38
Job time : 268 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 72 Seconds
(without alignments)
6866.152 Million cell updates/sec

Title: US-09-901-938-1
Perfect score: 1612
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52.6	3.3	423	1	US-08-187-780-2	Sequence 2, Appli
2	52.6	3.3	423	1	US-08-187-780-5	Sequence 5, Appli
3	52.6	3.3	423	2	US-08-478-485-2	Sequence 2, Appli
4	52.6	3.3	423	2	US-08-478-485-5	Sequence 5, Appli
5	52.6	3.3	423	4	US-08-478-486F-2	Sequence 2, Appli
6	52.6	3.3	423	4	US-08-478-486F-5	Sequence 5, Appli
7	52.6	3.3	528	4	US-08-478-486F-10	Sequence 10, Appl
8	52.6	3.3	599	6	5430019-1	Patent No. 5430019
9	52.6	3.3	618	4	US-08-478-486F-9	Sequence 9, Appli
10	52.6	3.3	1142	4	US-08-478-486F-11	Sequence 11, Appl
11	52.6	3.3	1219	5	PCT-US93-06251-11	Sequence 11, Appl
12	45.8	2.8	972	1	US-07-915-934-1	Sequence 1, Appli
13	45.8	2.8	972	1	US-08-325-743-1	Sequence 1, Appli
14	45.2	2.8	800	4	US-09-240-952-1	Sequence 1, Appli
15	45.2	2.8	1234	4	US-09-484-970B-167	Sequence 167, App
16	44.2	2.7	740	2	US-08-713-000-8	Sequence 8, Appli
17	44.2	2.7	740	2	US-08-975-316-8	Sequence 8, Appli
18	44.2	2.7	740	4	US-09-211-710-8	Sequence 8, Appli
19	44.2	2.7	740	4	US-09-615-192A-8	Sequence 8, Appli
20	44.2	2.7	741	2	US-08-975-316-58	Sequence 58, Appl
21	44.2	2.7	741	4	US-09-615-192A-58	Sequence 58, Appl
22	44.2	2.7	788	4	US-09-615-192A-96	Sequence 96, Appl
23	44.2	2.7	1875	5	PCT-US96-10618-1	Sequence 1, Appli
24	43.8	2.7	2852	3	US-09-027-137-2	Sequence 2, Appli
25	43.8	2.7	2852	4	US-09-344-441-2	Sequence 2, Appli
c 26	43.6	2.7	1481	2	US-08-474-379C-87	Sequence 87, Appl
c 27	43.6	2.7	3131	1	US-07-688-352C-21	Sequence 21, Appl
c 28	43.6	2.7	3131	3	US-09-146-249A-21	Sequence 21, Appl
c 29	43.6	2.7	3131	3	US-08-206-188B-21	Sequence 21, Appl
c 30	43.6	2.7	3131	5	PCT-US91-02714-20	Sequence 20, Appl
c 31	43.6	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
32	43.6	2.7	55827	4	US-09-813-133A-3	Sequence 3, Appli
33	43.2	2.7	3073	1	US-07-688-352C-31	Sequence 31, Appl
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36	43.2	2.7	3073	3	US-08-206-188B-31	Sequence 31, Appl
37	43.2	2.7	3073	5	PCT-US91-02714-30	Sequence 30, Appl
38	43	2.7	609	4	US-09-057-860A-1	Sequence 1, Appli
c 39	42.6	2.6	624	4	US-09-385-982-359	Sequence 359, App
40	42.4	2.6	3275	4	US-09-370-838-151	Sequence 151, App
41	42.2	2.6	1159	4	US-09-410-464-14	Sequence 14, Appl
42	42.2	2.6	5852	1	US-07-867-106-2	Sequence 2, Appli
43	42	2.6	540	3	US-08-643-704A-45	Sequence 45, Appl
44	42	2.6	11517	1	US-07-920-281C-1	Sequence 1, Appli
45	42	2.6	11517	4	US-08-466-277-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-187-780-2
; Sequence 2, Application US/08187780
; Patent No. 5459250
;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch,
;      MEDIUM TYPE:  360 Kb storage
;      COMPUTER:  IBM or IBM-compatible
;      OPERATING SYSTEM:  PC/MS-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/187,780
;      FILING DATE:  January 25, 1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howard M. Frankfort
;      REGISTRATION NUMBER:  32,613
;      REFERENCE/DOCKET NUMBER:  5986/13586-US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
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;     HYPOTHETICAL:  No
;     ANTI-SENSE:  No
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  This sequence can be
;       OTHER INFORMATION:  found on page 5, lines 3-13, in the
;       OTHER INFORMATION:  application, as filed.
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:  1-423
US-08-187-780-2

  Query Match           3.3%;  Score 52.6;  DB 1;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
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Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
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Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
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Db     194 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 253

Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
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Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337


RESULT 2
US-08-187-780-5
; Sequence 5, Application US/08187780
; Patent No. 5459250
;  GENERAL INFORMATION:
;     APPLICANT:  CLAUDIO BASILICO
;     APPLICANT:  DANIELA TALARICO
;     TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Darby & Darby P.C.
;       STREET:  805 Third Avenue
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10022
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 5.25 inch,
;       MEDIUM TYPE:  360 Kb storage
;       COMPUTER:  IBM or IBM-compatible
;       OPERATING SYSTEM:  PC/MS-DOS
;       SOFTWARE:  Wordperfect
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/187,780
;       FILING DATE:  January 25, 1994
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/901,705
;       FILING DATE:  June 22, 1992
;       APPLICATION NUMBER:  07/806,771
;       FILING DATE:  December 6, 1991
;       APPLICATION NUMBER:  07/177,506
;       FILING DATE:  April 4, 1988
;       APPLICATION NUMBER:  07/062,925
;       FILING DATE:  June 16, 1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Howard M. Frankfort
;       REGISTRATION NUMBER:  32,613
;       REFERENCE/DOCKET NUMBER:  5986/13586-US3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 527-7700
;       TELEFAX:  (212) 753-6237
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  423
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:
;       DESCRIPTION:  Genomic DNA
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  This sequence
;       OTHER INFORMATION:  corresponds to K-FGF-140 and can be
;       OTHER INFORMATION:  found on page 11, lines 39-47 and page
;       OTHER INFORMATION:  12, lines 1-31, in the application, as
;       OTHER INFORMATION:  filed.
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:  1-423
US-08-187-780-5

  Query Match           3.3%;  Score 52.6;  DB 1;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |    | ||||   | |  ||||| | |    | |
Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
           ||  | ||||    |||  | ||    | | |||    ||| | |||   ||    || |
Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
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Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
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Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337
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RESULT 3
US-08-478-485-2
; Sequence 2, Application US/08478485
; Patent No. 5883071
;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;      MEDIUM TYPE:  1.44 MB storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,485
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,780
;      FILING DATE:  January 25, 1994
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph R. Robinson
;      REGISTRATION NUMBER:  33,448
;      REFERENCE/DOCKET NUMBER:  5986/13586-US6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  This sequence can be
;      OTHER INFORMATION:  found on page 5, lines 3-13, in the
;      OTHER INFORMATION:  application, as filed.
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:  1-423
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US-08-478-485-2

  Query Match             3.3%;  Score 52.6;  DB 2;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |    | ||||   | |  |||| | |    | |
Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
           || | ||||    ||| | ||    | | |||    ||| | |||   ||    || |
Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
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Db     194 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 253

Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
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Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337


RESULT 4
US-08-478-485-5
; Sequence 5, Application US/08478485
; Patent No. 5883071
;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;      MEDIUM TYPE:  1.44 MB storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,485
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,780
;      FILING DATE:  January 25, 1994
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph R. Robinson
;      REGISTRATION NUMBER:  33,448
;      REFERENCE/DOCKET NUMBER:  5986/13586-US6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  423
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:
;       DESCRIPTION:  Genomic DNA
;     FEATURE:
;       NAME/KEY:
;       LOCATION:
;       IDENTIFICATION METHOD:
;       OTHER INFORMATION:  This sequence
;       OTHER INFORMATION:  corresponds to K-FGF-140 and can be
;       OTHER INFORMATION:  found on page 11, lines 39-47 and page
;       OTHER INFORMATION:  12, lines 1-31, in the application, as
;       OTHER INFORMATION:  filed.
;     PUBLICATION INFORMATION:
;       AUTHORS:
;       TITLE:
;       JOURNAL:
;       VOLUME:
;       ISSUE:
;       PAGES:
;       DATE:
;       DOCUMENT NUMBER:
;       FILING DATE:
;       PUBLICATION DATE:
;       RELEVANT RESIDUES IN SEQ ID NO:  1-423
US-08-478-485-5

  Query Match             3.3%;  Score 52.6;  DB 2;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |    | ||||   | |  |||||| | |    | |
Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
           ||  | ||||    |||  | ||    | | |||    ||| | |||   ||    || |
Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
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Db     194 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 253

Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
           ||  |   ||  | |||| |||| |  |        ||    |||   ||| ||| ||||
Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337


RESULT 5
US-08-478-486F-2
; Sequence 2, Application US/08478486F
; Patent No. 6432702
;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;      MEDIUM TYPE:  1.44 MB storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC/MS-DOS
;       SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,486F
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,780
;      FILING DATE:  January 25, 1994
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howard M. Frankfort
;      REGISTRATION NUMBER:  32,613
;      REFERENCE/DOCKET NUMBER:  5986/13586-US7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  This sequence can be
;      OTHER INFORMATION:  found on page 5, lines 3-13, in the
;      OTHER INFORMATION:  application, as filed.
US-08-478-486F-2

  Query Match             3.3%;  Score 52.6;  DB 4;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |    | ||||   | |  |||||| | |    | |
Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
           ||  | ||||    |||  | ||    | | |||    ||| | |||   ||    || |
Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
           ||   ||| |    | | |   ||||     ||  ||||| | | ||| || | ||  |
Db     194 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 253

Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
           ||  |   ||  | |||| |||| |  |        ||    |||   ||| ||| ||||
Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337


RESULT 6
US-08-478-486F-5
; Sequence 5, Application US/08478486F
; Patent No. 6432702
```

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;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;      MEDIUM TYPE:  1.44 MB storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,486F
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,780
;      FILING DATE:  January 25, 1994
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howard M. Frankfort
;      REGISTRATION NUMBER:  32,613
;      REFERENCE/DOCKET NUMBER:  5986/13586-US7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Genomic DNA
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:  This sequence
;      OTHER INFORMATION:  corresponds to K-FGF-140 and can be
;      OTHER INFORMATION:  found on page 11, lines 39-47 and page
;      OTHER INFORMATION:  12, lines 1-31, in the application, as
;      OTHER INFORMATION:  filed.
US-08-478-486F-5

  Query Match             3.3%;  Score 52.6;  DB 4;  Length 423;
  Best Local Similarity   52.4%;  Pred. No. 0.00016;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |     | ||||   | |  |||||| | |     | |
Db      74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
           ||  | ||||    |||  | ||    | | |||    |||  | |||   ||    || |
Db     134 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 193

Qy     409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
           ||   ||| |    | | |   ||||     ||  |||||  | | ||| || | ||  |

Db     194 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 253

Qy     469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
           ||  |   ||  | |||| |||| | |        ||     |||   ||| ||| ||||
Db     254 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 310

Qy     529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
           | ||     |||| | |  | || |||
Db     311 AGTCCTACAAGTACCCCGGCATGTTCA 337


RESULT 7
US-08-478-486F-10
; Sequence 10, Application US/08478486F
; Patent No. 6432702
;  GENERAL INFORMATION:
;    APPLICANT:  CLAUDIO BASILICO
;    APPLICANT:  DANIELA TALARICO
;    TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby P.C.
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;      MEDIUM TYPE:  1.44 MB storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC/MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,486F
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,780
;      FILING DATE:  January 25, 1994
;      APPLICATION NUMBER:  07/901,705
;      FILING DATE:  June 22, 1992
;      APPLICATION NUMBER:  07/806,771
;      FILING DATE:  December 6, 1991
;      APPLICATION NUMBER:  07/177,506
;      FILING DATE:  April 4, 1988
;      APPLICATION NUMBER:  07/062,925
;      FILING DATE:  June 16, 1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Howard M. Frankfort
;      REGISTRATION NUMBER:  32,613
;      REFERENCE/DOCKET NUMBER:  5986/13586-US7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 527-7700
;      TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  528 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-478-486F-10

  Query Match             3.3%;  Score 52.6;  DB 4;  Length 528;
  Best Local Similarity   52.4%;  Pred. No. 0.00018;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy     289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
           | | | ||| |||||| |||   | |     | ||||   | |  ||||| | |     | |
Db     182 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 241

Qy     349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
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Db    242 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 301

Qy    409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468

Db    302 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 361

Qy    469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528

Db    362 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 418

Qy    529 ACTCTCCTCAGTATCACTTCCTGGTCA 555

Db    419 AGTCCTACAAGTACCCCGGCATGTTCA 445


RESULT 8
5430019-1
;Patent No. 5430019
;     APPLICANT: ROGERS, DAVID T.;WOLFMAN, NEIL M.;SEEHRA, JASBIR S.
;     TITLE OF INVENTION: HOMOGENEOUS K-FGF AND USE OF THE SAME
;     NUMBER OF SEQUENCES: 2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/898,051
;       FILING DATE: 12-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 438,278
;       FILING DATE: 16-NOV-1989
;SEQ ID NO:1:
;       LENGTH: 599
5430019-1

  Query Match             3.3%;  Score 52.6;  DB 6;  Length 599;
  Best Local Similarity   52.4%;  Pred. No. 0.00019;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy    289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348

Db    185 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 244

Qy    349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408

Db    245 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 304

Qy    409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468

Db    305 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 364

Qy    469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528

Db    365 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 421

Qy    529 ACTCTCCTCAGTATCACTTCCTGGTCA 555

Db    422 AGTCCTACAAGTACCCCGGCATGTTCA 448


RESULT 9
US-08-478-486F-9
; Sequence 9, Application US/08478486F
; Patent No. 6432702
;  GENERAL INFORMATION:
;     APPLICANT:  CLAUDIO BASILICO
;     APPLICANT:  DANIELA TALARICO
;     TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Darby & Darby P.C.
;       STREET:  805 Third Avenue
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10022
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;       MEDIUM TYPE:  1.44 MB storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC/MS-DOS
;       SOFTWARE:  Wordperfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/478,486F
;       FILING DATE:  June 7, 1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/187,780
;       FILING DATE:  January 25, 1994
;       APPLICATION NUMBER:  07/901,705
;       FILING DATE:  June 22, 1992
;       APPLICATION NUMBER:  07/806,771
;       FILING DATE:  December 6, 1991
;       APPLICATION NUMBER:  07/177,506
;       FILING DATE:  April 4, 1988
;       APPLICATION NUMBER:  07/062,925
;       FILING DATE:  June 16, 1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Howard M. Frankfort
;       REGISTRATION NUMBER:  32,613
;       REFERENCE/DOCKET NUMBER:  5986/13586-US7
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 527-7700
;       TELEFAX:  (212) 753-6237
;  INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  618
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-478-486F-9

  Query Match             3.3%;  Score 52.6;  DB 4;  Length 618;
  Best Local Similarity   52.4%;  Pred. No. 0.00019;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy    289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348

Db    272 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 331

Qy    349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408

Db    332 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 391

Qy    409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468

Db    392 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 451

Qy    469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528

Db    452 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 508

Qy    529 ACTCTCCTCAGTATCACTTCCTGGTCA 555

Db    509 AGTCCTACAAGTACCCCGGCATGTTCA 535


RESULT 10
US-08-478-486F-11
; Sequence 11, Application US/08478486F
; Patent No. 6432702
;  GENERAL INFORMATION:
;     APPLICANT:  CLAUDIO BASILICO
;     APPLICANT:  DANIELA TALARICO
;     TITLE OF INVENTION:  MAMMALIAN GROWTH FACTOR
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Darby & Darby P.C.
;       STREET:  805 Third Avenue
```

```
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  10022
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Diskette, 3+ inch,
;       MEDIUM TYPE:  1.44 MB storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC/MS-DOS
;       SOFTWARE:  Wordperfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/478,486F
;       FILING DATE:  June 7, 1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/187,780
;       FILING DATE:  January 25, 1994
;       APPLICATION NUMBER:  07/901,705
;       FILING DATE:  June 22, 1992
;       APPLICATION NUMBER:  07/806,771
;       FILING DATE:  December 6, 1991
;       APPLICATION NUMBER:  07/177,506
;       FILING DATE:  April 4, 1988
;       APPLICATION NUMBER:  07/062,925
;       FILING DATE:  June 16, 1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Howard M. Frankfort
;       REGISTRATION NUMBER:  32,613
;       REFERENCE/DOCKET NUMBER:  5986/13586-US7
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 527-7700
;       TELEFAX:  (212) 753-6237
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1142 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Genomic DNA
US-08-478-486F-11

  Query Match             3.3%;  Score 52.6;  DB 4;  Length 1142;
  Best Local Similarity   52.4%;  Pred. No. 0.00027;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy    289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
          | | | ||| |||||| |||   | |    | ||||   | |  ||||| | |    | |
Db    514 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 573

Qy    349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
          ||  | ||||  . |||  | ||    | | |||    ||| | |||   ||    || | |
Db    574 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 633

Qy    409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
          ||   ||| |    | | |   ||||     ||  |||||  | | ||| || | ||  |
Db    634 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 693

Qy    469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
          ||  |   ||  | |||| |||| | |  |        ||    |||  ||| ||| ||||
Db    694 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 750

Qy    529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
          | ||     |||| | |  | || |||
Db    751 AGTCCTACAAGTACCCCGGCATGTTCA 777


RESULT 11
PCT-US93-06251-11
; Sequence 11, Application PC/TUS9306251
;  GENERAL INFORMATION:
;     APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;     TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;     TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;     NUMBER OF SEQUENCES:  93
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/06251
;       FILING DATE:  19930630
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  8586
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  516-742-4343
;       TELEFAX:  516-742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1219 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-11

  Query Match             3.3%;  Score 52.6;  DB 5;  Length 1219;
  Best Local Similarity   52.4%;  Pred. No. 0.00028;
  Matches  140;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy    289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
          | | | ||| |||||| |||   | |    | ||||   | |  ||||| | |    | |
Db    591 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 650

Qy    349 CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
          ||  | ||||    |||  | ||    | | |||    ||| | |||   ||    || | |
Db    651 CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCG 710

Qy    409 TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
          ||   ||| |    | | |   ||||     ||  |||||  | | ||| || | ||  |
Db    711 TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 770

Qy    469 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACC 528
          ||  |   ||  | |||| |||| | |  |        ||    |||  ||| ||| ||||
Db    771 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG 827

Qy    529 ACTCTCCTCAGTATCACTTCCTGGTCA 555
          | ||     |||| | |  | || |||
Db    828 AGTCCTACAAGTACCCCGGCATGTTCA 854


RESULT 12
US-07-915-934-1
; Sequence 1, Application US/07915934
; Patent No. 5360893
;  GENERAL INFORMATION:
;     APPLICANT:  OWENS, GREGORY P.
;     APPLICANT:  COHEN, J. J.
;     APPLICANT:  HAHN, WILLIAM E.
;     TITLE OF INVENTION:  DNA SEQUENCES ENCODING PROTEINS USED TO
;     TITLE OF INVENTION:  ELICIT AND DETECT PROGRAMMED CELL DEATH
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FREDERICK W. PEPPER, PH.D.
;       STREET:  11545 W. BERNARDO COURT, STE. 302
```

```
;       CITY:  SAN DIEGO
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92127
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/915,934
;       FILING DATE:  19920720
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PEPPER PH.D., FREDERICK W.
;       REGISTRATION NUMBER:  31,286
;       REFERENCE/DOCKET NUMBER:  92-0224.02
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 451-1120
;       TELEFAX:  (619) 451-9628
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  972 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..864
US-07-915-934-1

  Query Match             2.8%;  Score 45.8;  DB 1;  Length 972;
  Best Local Similarity   67.0%;  Pred. No. 0.015;
  Matches   65;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy   1178 GAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTA 1237
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Db    863 GAAAGGTGTTAAATTCTTAAAAATAAATGTTCCTTATGCCTCACTACCTCAAAAAAAAAA 922

Qy   1238 AGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
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Db    923 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 959


RESULT 13
US-08-325-743-1
; Sequence 1, Application US/08325743
; Patent No. 5527682
;  GENERAL INFORMATION:
;    APPLICANT:  OWENS, GREGORY P.
;    APPLICANT:  COHEN, J. J.
;    APPLICANT:  HAHN, WILLIAM E.
;    TITLE OF INVENTION:  DNA SEQUENCES ENCODING PROTEINS USED TO
;    TITLE OF INVENTION:  ELICIT AND DETECT PROGRAMMED CELL DEATH
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FREDERICK W. PEPPER, PH.D.
;      STREET:  11545 W. BERNARDO COURT, STE. 302
;      CITY:  SAN DIEGO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92127
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/325,743
;      FILING DATE:  19-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/915,934
;      FILING DATE:  20-JUL-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PEPPER PH.D., FREDERICK W.
;      REGISTRATION NUMBER:  31,286
;      REFERENCE/DOCKET NUMBER:  92-0224.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 451-1120
;      TELEFAX:  (619) 451-9628
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  972 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..864
US-08-325-743-1

  Query Match             2.8%;  Score 45.8;  DB 1;  Length 972;
  Best Local Similarity   67.0%;  Pred. No. 0.015;
  Matches   65;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy   1178 GAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTA 1237
          || | | | |   | |  | | ||   | |||||| |||||| |  | | |  |     |
Db    863 GAAAGGTGTTAAATTCTTAAAAATAAATGTTCCTTATGCCTCACTACCTCAAAAAAAAAA 922

Qy   1238 AGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
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Db    923 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 959


RESULT 14
US-09-240-952-1
; Sequence 1, Application US/09240952
; Patent No. 6331523
;  GENERAL INFORMATION:
;    APPLICANT:  Kljavin, Ivar
;    APPLICANT:  La Fleur, Monique
;    TITLE OF INVENTION:  Method of Preventing the Death of Retinal
;    TITLE OF INVENTION:  Neurons and Treating Ocular Diseases
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/240,952
;      FILING DATE:  29-Jan-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/041,383
;      FILING DATE:  12-Mar-98
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1088P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  800 base pairs
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;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
US-09-240-952-1

  Query Match             2.8%;  Score 45.2;  DB 4;  Length 800;
  Best Local Similarity   50.0%;  Pred. No. 0.02;
  Matches  141;  Conservative    0;  Mismatches  138;  Indels    3;  Gaps    1;

Qy     251 CTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGAT 310
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Qy     311 CCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGAT 370
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Db     274 CTACCCGGATGGCAAAGTCAATGGATCCCACGAAGCCAATATGTTAAGTGTTTTGGAAAT 333

Qy     371 CAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTG 430
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Db     334 ATTTGCTGTGTCTCAGGGGATTGTAGGAATACGAGGAGTTTTCAGCAACAAATTTTTAGC 393

Qy     431 CATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT 490
           |||      | ||| ||  |   || |     | | |||    | ||  |||||| |||
Db     394 GATGTCAAAAAAAGGAAAACTCCATGCAAGTGCCAAGTTCA---CAGATGACTGCAAGTT 450

Qy     491 CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
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Db     451 CAGGGAGCGTTTTCAAGAAAATAGCTATAATACCTATGCCTC 492


RESULT 15
US-09-484-970B-167
; Sequence 167, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Karen A.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Walker, Michael G.
;  TITLE OF INVENTION:  BONE REMODELING GENES
;  FILE REFERENCE:  PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE:  2000-01-18
;  NUMBER OF SEQ ID NOS:  172
;  SOFTWARE:  PERL Program
; SEQ ID NO 167
;   LENGTH: 1234
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6426186 333034.1
US-09-484-970B-167

  Query Match             2.8%;  Score 45.2;  DB 4;  Length 1234;
  Best Local Similarity   50.0%;  Pred. No. 0.025;
  Matches  141;  Conservative    0;  Mismatches  138;  Indels    3;  Gaps    1;

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Db     499 CTCGGGGCGCCGGACCGGCAGCCTCTACTGCAGAGTGGGCATCGGTTTCCATCTGCAGAT 558

Qy     311 CCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGAT 370
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Db     559 CTACCCGGATGGCAAAGTCAATGGATCCCACGAAGCCAATATGTTAAGTGTTTTGGAAAT 618

Qy     371 CAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTG 430
           | | |  |   ||  |||| |  ||   ||| ||  | ||||  | ||   |
Db     619 ATTTGCTGTGTCTCAGGGGATTGTAGGAATACGAGGAGTTTTCAGCAACAAATTTTTAGC 678

Qy     431 CATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT 490
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Qy     491 CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
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Search completed: May 29, 2003, 00:07:03
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GenCore version 5.1.4_p5_4578

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Run on: May 28, 2003, 21:20:14 ; Search time 4519 Seconds
(without alignments)
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Title: US-09-901-938-1
Perfect score: 1612
Sequence: 1 cggcaaaaaggagggaatcc.....tgagcaccttctgtctcgct 1612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	798	49.5	996	6	AX464132	AX464132 Sequence
7	756	46.9	756	6	AX249749	AX249749 Sequence
8	756	46.9	756	6	AX250102	AX250102 Sequence
9	756	46.9	756	6	AX481467	AX481467 Sequence
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c 19	234.2	14.5	204909	2	AC130862	AC130862 Rattus no
c 20	230.8	14.3	178533	2	AC015538	AC015538 Mus muscu
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23	73.2	4.5	624	6	AX191715	AX191715 Sequence
24	72.8	4.5	514	6	AX097639	AX097639 Sequence
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26	72.6	4.5	651	9	AB018122	AB018122 Homo sapi
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39	72.4	4.5	882	6	AX191713	AX191713 Sequence
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42	72.4	4.5	1117	6	AX351022	AX351022 Sequence
43	72.4	4.5	1190	6	AX275042	AX275042 Sequence
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45	68.4	4.2	633	10	AB025718	AB025718 Mus muscu

ALIGNMENTS

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LOCUS AF263537 1612 bp mRNA linear PRI 14-DEC-2000
DEFINITION Homo sapiens FGF23 (FGF23) mRNA, complete cds.
ACCESSION AF263537
VERSION AF263537.1 GI:9964291
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1612)
AUTHORS White,K.E., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,
Lorenz-Depiereux,B., Grabowski,M., Meitinger,T. and Strom,T.M.
TITLE Autosomal dominant hypophosphataemic rickets is associated with

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            mutations in FGF23
  JOURNAL   Nat. Genet. 26 (3), 345-348 (2000)
  MEDLINE   20517346
   PUBMED   11062477
REFERENCE   2  (bases 1 to 1612)
  AUTHORS   Strom,T.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAY-2000) Medizinische Genetik, Goethestr. 29,
            Muenchen 80336, Germany
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     gene            1. .1612
                     /gene="FGF23"
     CDS             147. .902
                     /gene="FGF23"
                     /codon_start=1
                     /product="FGF23"
                     /protein_id="AAG09917.1"
                     /db_xref="GI:9964292"
                     /translation="MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYT
                     ATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI
                     FGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSR
                     RNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSP
                     MASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI"
BASE COUNT      405 a    462 c    418 g    327 t
ORIGIN

  Query Match             100.0%;  Score 1612;  DB 9;  Length 1612;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1612;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 AAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCA 120
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Db     121 GCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTG 180

Qy     181 CCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGC 240
Db     181 CCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGC 240

Qy     241 TCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACC 300
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Db     601 CCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCC 660

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Qy     721 TGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGA 780
Db     721 TGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGA 780

Qy     781 GCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAG 840
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Qy    1021 TGCTTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGT 1080
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Qy    1081 CATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCA 1140
Db    1081 CATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCA 1140

Qy    1141 ACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATA 1200
Db    1141 ACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATA 1200

Qy    1201 TTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAA 1260
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Qy    1261 AAAAAAAAAAAAAAAGCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGA 1320
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Qy    1321 AATCGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCC 1380
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Qy    1381 CACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAA 1440
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Qy    1441 ACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGAC 1500
Db    1441 ACACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGCTGTCAAAAGAC 1500

Qy    1501 TGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGA 1560
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Qy    1561 ATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1612
Db    1561 ATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1612

RESULT 2
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DEFINITION  Homo sapiens hypf mRNA for tumor-derived hypophosphatemia inducing
            factor, complete cds.
ACCESSION   AB047858
VERSION     AB047858.1  GI:14196226
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Shimada,T., Mizutani,S., Muto,T., Yoneya,T., Hino,R., Takeda,S.,
            Takeuchi,Y., Fujita,T., Fukumoto,S. and Yamashita,T.
  TITLE     Cloning and characterization of FGF23 as a causative factor of
            tumor-induced osteomalacia
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (11), 6500-6505 (2001)
  MEDLINE   21267444
REFERENCE   2  (bases 1 to 3004)
  AUTHORS   Yamashita,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2000) Takeyoshi Yamashita, Kirin Brewery Co.,
            Ltd., Pharmaceutical Research Lab.; Miyahara 3, Takasaki, Gunma
            370-1295, Japan (E-mail:tyamashita@kirin.co.jp, Tel:81273469789,
            Fax:81273461672)
FEATURES             Location/Qualifiers
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BASE COUNT      812 a    731 c    672 g    789 t
ORIGIN
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Query Match 99.1%; Score 1598; DB 9; Length 3004;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 GAATCCAGTCTAGGATCCTCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAG 60

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Db     121 GAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTC 180

Qy     195 TGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGG 254
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Db     481 CACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTC 540

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Db     781 AGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCT 840

Qy     855 GGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAG 914
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Db     841 GGGGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAG 900

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Db     961 ACGTTCCGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGT 1020

Qy    1035 CCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACC 1094
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Qy    1155 AATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGT 1214
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Db    1141 AATTTCCCCTTCATGAAGGTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGT 1200

Qy    1215 GCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
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Db    1201 GCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1260

Qy    1275 GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCA 1334
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Qy    1335 GAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAG 1394
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Qy    1515 TGAAAACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAATAGAAAA 1574
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RESULT 3
AX191707
LOCUS       AX191707                1211 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 1 from Patent WO0149740.
ACCESSION   AX191707
VERSION     AX191707.1  GI:15209882
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1211)
  AUTHORS   Conklin,D.C.
  TITLE     Novel fgf homolog zfgf12
  JOURNAL   Patent: WO 0149740-A 1 12-JUL-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           75.1%;  Score 1211;  DB 6;  Length 1211;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1211;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 92
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Db       1 TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC 60

Qy      93 CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 152
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Db     121 GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC 180

Qy     213 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 272
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Db     181 AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG 240

Qy     273 TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT 332
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Qy     573 AGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAAC 632
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Db     781 CCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCGGAA 840

Qy     873 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 932
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Db     841 GGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCCA 900

Qy     933 TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA 992
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Qy     993 AGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC 1052
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Qy    1053 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1112
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Db    1021 TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1080

Qy    1113 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1172
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Db    1081 AGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAG 1140

Qy    1173 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1232
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Db    1141 GTAGAGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC 1200

Qy    1233 TTTTAAGCATA 1243
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Db    1201 TTTTAAGCATA 1211


RESULT 4
AC008012
LOCUS       AC008012                170200 bp    DNA     linear   PRI 15-MAR-2002
DEFINITION  Homo sapiens 12p13 BAC RPCI11-388F6 (Roswell Park Cancer Institute
            Human BAC Library) complete sequence.
ACCESSION   AC008012
VERSION     AC008012.8  GI:5762548
KEYWORDS    HTG.
SOURCE      Homo sapiens.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 170200)
AUTHORS Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H., Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S., Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W., Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A., Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L., Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M., Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 170200)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 170200)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 170200)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 5 (bases 1 to 170200)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 6 (bases 1 to 170200)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Aug 24, 1999 this sequence version replaced gi:5708398.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT----------

---------- Summary Statistics ----------

Contig length:	170200
Phrap values in estimate:	169098
Average error rate (BCM-Phrap estimate):	0.000234169
Fraction of Phrap values less than 40 :	0.0503199
Number of consensus changing edits:	21
Number of N's in consensus :	0

---------- Consensus changing edits ----------

Position	Original+Context	Edited+Context
14775	attccaaaaa(n)ttatatactg	attccaaaaa(t)ttatatactg
33904	ggaaacaaca(n)aaaaagaccc	ggaaacaaca(a)aaaaagaccc
50944	tacttaacat(n)tcttctcttt	tacttaacat(t)tcttctcttt
51576	cttatagtat(n)tgttaggtgg	cttatagtat(t)tgttaggtgg
56619	aactatatga(n)acccagctgg	aactatatga(a)acccagctgg
97197	gcagccatct(n)tcaaccacgg	gcagccatct(t)tcaaccacgg
97501	tcatgcctgt(g)atcccagcac	tcatgcctgt(a)atcccagcac
99719	atatatatat(n)tntttagtgg	atatatatat(t)tttttagtgg
99721	atatatatnt(n)tttagtggag	atatatattt(t)tttagtggag
101544	aggtgaaaca(n)caaggaagta	aggtgaaaca(a)caaggaagta
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136219	ccctaaagtg(n)tttctttctt	ccctaaagtg(t)tttctttctt
136246	tttctttttt(n)ttttttaag	tttctttttt(t)ttttttaag
154830	atctctacta(n)aaatacanna	atctctacta(a)aaatacaaaa
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154839	anaaatacan(n)aaattagccg	aaaaatacaa(a)aaattagccg
164836	ttttcttctt(n)taatgtgtct	ttttcttctt(t)taatgtgtct
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164929	atggaatagt(n)tcagtaggat	atggaatagt(t)tcagtaggat
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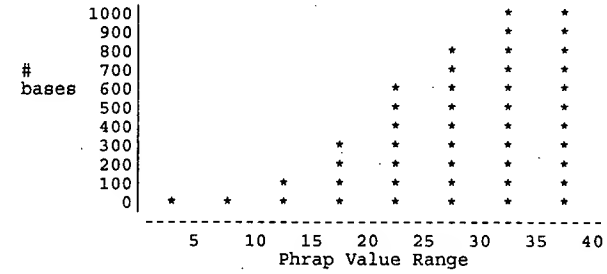
--------- Distribution of Quality < 40 Bases ----------



Version: 1.01 xfqo.

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Db  134664 GGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGC 134723

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RESULT 5
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LOCUS       AX403623                996 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 510 from Patent WO0073454.
ACCESSION   AX403623
VERSION     AX403623.1  GI:21437088
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
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           Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
           Williams,P., Wood,W.I. and Zhang,Z.
  TITLE    Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL  Patent: WO 0073454-A 510 07-DEC-2000;
           Genentech Inc. (US)
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  Matches  798;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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ACCESSION   AX464132
VERSION     AX464132.1  GI:21899082
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SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0140466-A 265 07-JUN-2001;
            Genentech Inc. (US)
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Qy     114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCTCAGGCTCTGG 173
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RESULT 7
AX249749
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DEFINITION  Sequence 3 from Patent WO0166596.
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VERSION     AX249749.1  GI:15864369
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Itoh,N. and Kavanaugh,M.W.
  TITLE     Human fgf-23 gene and gene expression products
  JOURNAL   Patent: WO 0166596-A 3 13-SEP-2001;
            CHIRON CORPORATION (US) ; Kyoto University (JP)
FEATURES             Location/Qualifiers
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Qy    747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
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Db    601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy    807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
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Db    661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy    867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
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Db    721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756


RESULT 8
AX250102
LOCUS       AX250102                 756 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 3 from Patent WO0166595.
ACCESSION   AX250102
VERSION     AX250102.1  GI:15864511
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Itoh,N. and Kavanaugh,M.W.
  TITLE     Human fgf-23 gene and gene expression products
  JOURNAL   Patent: WO 0166595-A 3 13-SEP-2001;
            CHIRON CORPORATION (US) ; Kyoto University (JP)
FEATURES             Location/Qualifiers
     source          1. .756
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      159 a    250 c    212 g    135 t
ORIGIN

  Query Match             46.9%;  Score 756;  DB 6;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-171;
  Matches  756;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
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Db      1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
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Db     61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy    267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
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Db    121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy    327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
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Db    181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy    387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
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Db    241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy    447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
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Db    301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360
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Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
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Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
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Db     421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
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Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
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Db     541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
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Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
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Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
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Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
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RESULT 9
AX481467
LOCUS       AX481467                 756 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 81 from Patent WO02055693.
ACCESSION   AX481467
VERSION     AX481467.1  GI:22316381
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P.
  TITLE     Method for inhibiting the expression of a target gene
  JOURNAL   Patent: WO 02055693-A 81 18-JUL-2002;
            Ribopharma AG (DE)
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     source          1. .756
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                     /db_xref="taxon:9606"
BASE COUNT      159 a    250 c    212 g    135 t
ORIGIN

  Query Match           46.9%;  Score 756;  DB 6;  Length 756;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-171;
  Matches  756;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
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Db       1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy     207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
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Qy     267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
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Db     121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy     327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240
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Qy     387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
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Db     241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy     507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
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Db     361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
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Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
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Db     481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy     687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
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Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
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Db     601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
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Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||||||||||||||||||||||||||||||||||
Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756
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RESULT 10
AB037973
LOCUS       AB037973                 756 bp    mRNA    linear   PRI 11-NOV-2000
DEFINITION  Homo sapiens FGF23 mRNA for FGF-23, complete cds.
ACCESSION   AB037973
VERSION     AB037973.1  GI:10119773
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Yamashita,T., Yoshioka,M. and Itoh,N.
  TITLE     Identification of a novel fibroblast growth factor, FGF-23,
            preferentially expressed in the ventrolateral thalamic nucleus of
            the brain
  JOURNAL   Biochem. Biophys. Res. Commun. 277 (2), 494-498 (2000)
  MEDLINE   20490027
REFERENCE   2  (bases 1 to 756)
  AUTHORS   Itoh,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2000) Nobuyuki Itoh, Kyoto University, Graduate
            School of Pharmaceutical Sciences, Department of Genetic
            Biochemistry; Yoshida-Shimoadachi, Sakyo, Kyoto, Kyoto 606-8501,
            Japan (E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540,
            Fax:81-75-753-4600)
FEATURES             Location/Qualifiers
     source          1. .756
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                     /db_xref="taxon:9606"
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BASE COUNT      159 a    250 c    212 g    135 t
ORIGIN

  Query Match           46.9%;  Score 756;  DB 9;  Length 756;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-171;
  Matches  756;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
Db      1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
Db     61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy    267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
Db    121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy    327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
Db    181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy    387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
Db    241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy    447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
Db    301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy    507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
Db    361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy    567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
Db    421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy    627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
Db    481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy    687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
Db    541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy    747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
Db    601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660

Qy    807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
Db    661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy    867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
Db    721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 756


RESULT 11
AX235431
LOCUS       AX235431                753 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 1 from Patent WO0161007.
ACCESSION   AX235431
VERSION     AX235431.1  GI:15593931
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Luethy,R., Yang,R., Suggs,S. and Sarosi,I.
  TITLE     Fibroblast growth factor-23 molecules and uses thereof
  JOURNAL   Patent: WO 0161007-A 1 23-AUG-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           46.7%;  Score 753;  DB 6;  Length 753;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-171;
  Matches  753;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
Db      1 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
Db     61 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 120

Qy    267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
Db    121 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 180

Qy    327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
Db    181 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 240

Qy    387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
Db    241 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 300

Qy    447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
Db    301 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 360

Qy    507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
Db    361 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 420

Qy    567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
Db    421 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 480

Qy    627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
Db    481 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 540

Qy    687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
Db    541 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 600

Qy    747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
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Db     661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATC 899
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Db     721 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATC 753


RESULT 12
AX191709
LOCUS       AX191709                753 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 3 from Patent WO0149740.
ACCESSION   AX191709
VERSION     AX191709.1  GI:15209884
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Conklin,D.C.
  TITLE     Novel fgf homolog zfgf12
  JOURNAL   Patent: WO 0149740-A 3 12-JUL-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT      108 a     90 c    132 g     94 t    329 others
ORIGIN

  Query Match           32.8%;  Score 528;  DB 6;  Length 753;
  Best Local Similarity   56.3%;  Pred. No. 1.4e-116;
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Qy     147 ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
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Qy     447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
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Db     361 GARAAYGGNTAYGAYGTNTAYCAYWSNCCNCARTAYCAYTTYYTNGTNWSNYTNGGNMGN 420

Qy     567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
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Db     421 GCNAARMGNGCNTTYYTNCCNGGNATGAAYCCNCCNCCNTAYWSNCARTTYYTNWSNMGN 480

Qy     627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
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Db     481 MGNAAYGARATHCCNYTNATHCAYTTYAAYACNCCNATHCCNMGNMGNCAYACNMGNWSN 540

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Db     541 GCNGARGAYGAYWSNGARMGNGAYCCNYTNAAYGTNYTNAARCCNMGNGCNMGNATGACN 600

Qy     747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
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Db     601 CCNGCNCCNGCNWSNTGYWSNCARGARYTNCCNWSNGCNGARGAYAAYWSNCCNATGGCN 660

Qy     807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
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Db     661 WSNGAYCCNYTNGGNGTNGTNMGNGGNGGNMGNGTNAAYACNCAYGCNGGNGGNACNGGN 720

Qy     867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATC 899
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Db     721 CCNGARGGNTGYMGNCCNTTYGCNAARTTYATH 753


RESULT 13
AF263536
LOCUS       AF263536                1559 bp    mRNA    linear   ROD 14-DEC-2000
DEFINITION  Mus musculus FGF23 (Fgf23) mRNA, complete cds.
ACCESSION   AF263536
VERSION     AF263536.1  GI:9964289
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1559)
  AUTHORS   White,K.E., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,
            Lorenz-Depiereux,B., Grabowski,M., Meitinger,T. and Strom,T.M.
  TITLE     Autosomal dominant hypophosphataemic rickets is associated with
            mutations in FGF23
  JOURNAL   Nat. Genet. 26 (3), 345-348 (2000)
  MEDLINE   20517346
   PUBMED   11062477
REFERENCE   2  (bases 1 to 1559)
  AUTHORS   Strom,T.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAY-2000) Medizinische Genetik, Goethestr. 29,
            Muenchen 80336, Germany
FEATURES             Location/Qualifiers
     source          1. .1559
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                     /db_xref="taxon:10090"
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     gene            1. .1559
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                     AASDPLGVLRRGRGDARGGAGGADRCRPFPRFV"
BASE COUNT      347 a    457 c    405 g    350 t
ORIGIN

  Query Match           28.4%;  Score 457.4;  DB 10;  Length 1559;
  Best Local Similarity   73.0%;  Pred. No. 1.8e-99;
  Matches  602;  Conservative    0;  Mismatches  221;  Indels    2;  Gaps    1;

Qy      99 GGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCC 158
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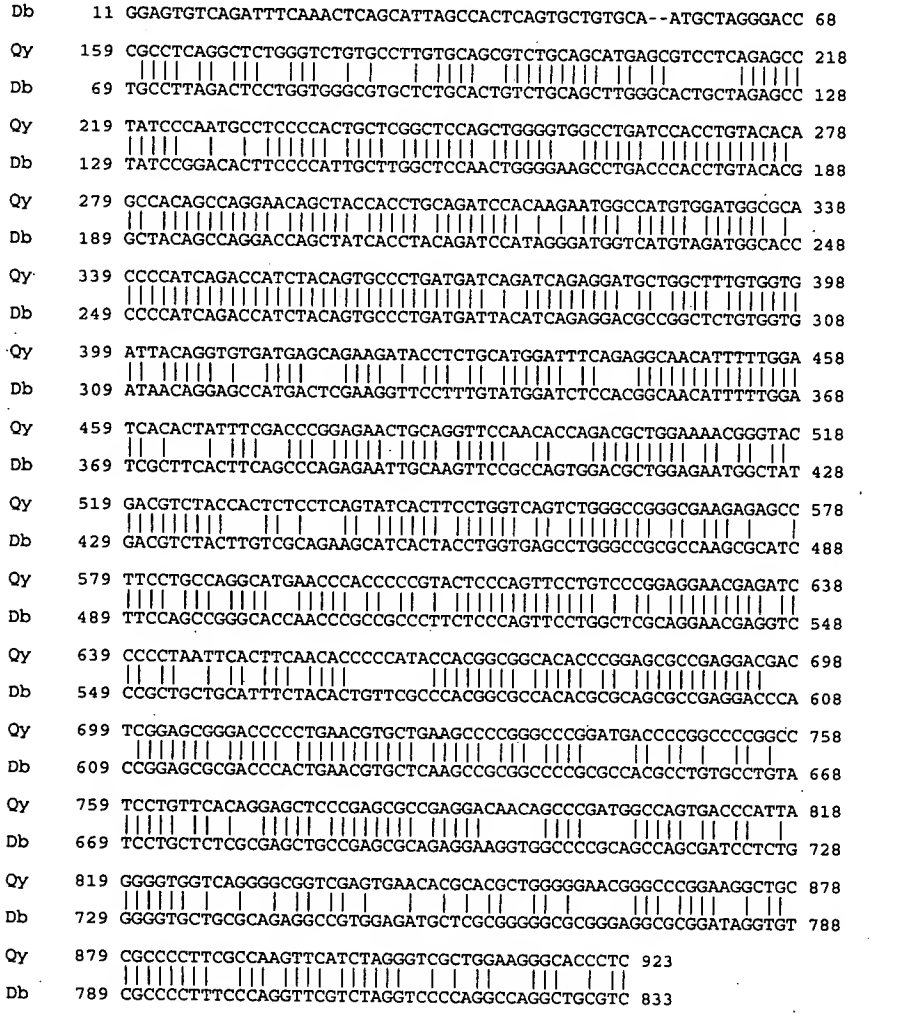

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LOCUS       AB078777                 756 bp    mRNA    linear   ROD 26-JAN-2002
DEFINITION  Rattus norvegicus FGF23 mRNA for fibroblast growth factor 23,
            complete cds.
ACCESSION   AB078777
VERSION     AB078777.1  GI:18376670
KEYWORDS    .
SOURCE      Rattus norvegicus cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Itoh,N.
  TITLE     Rattus norvegicus fgf23
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 756)
  AUTHORS   Itoh,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Nobuyuki Itoh, Kyoto University Graduate
            School of Pharmaceutical Sciences, Department of Genetic
            Biochemistry; Yoshida-Shimoadachi, Sakyo, Kyoto 606-8501, Japan
            (E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540,
            Fax:81-75-753-4600)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10116"
     gene            1. .756
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     CDS             1. .756
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ORIGIN
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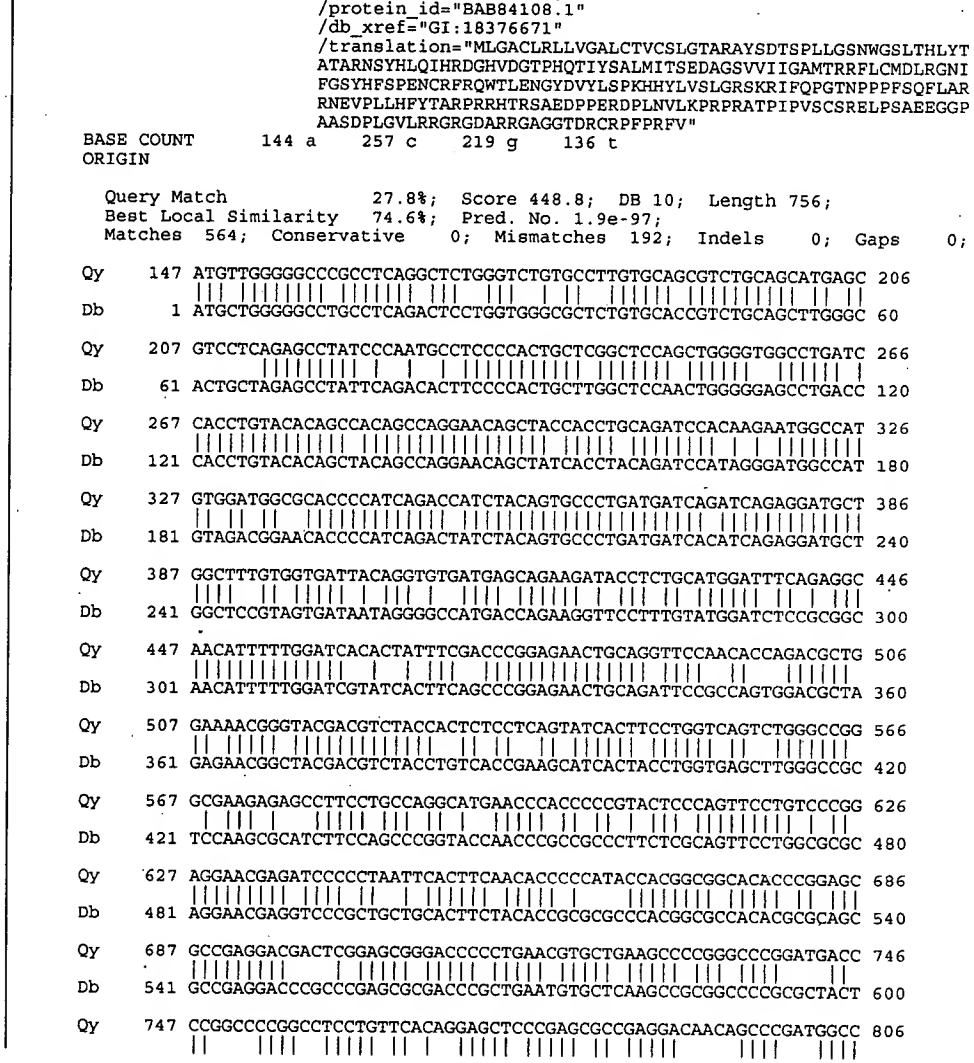

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Db    661 AGCGACCCCCTGGGAGTGCTGCGCAGAGGCCGCGGGGATGCTCGCCGGGGCGCGGGAGGC 720

Qy    867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||  | || ||||||||  ||| |||| |||||
Db    721 ACGGATCGGTGTCGCCCCTTTCCCAGGTTCGTCTAG 756


RESULT 15
AX249747
LOCUS       AX249747                 756 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 1 from Patent WO0166596.
ACCESSION   AX249747
VERSION     AX249747.1  GI:15864368
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 756)
  AUTHORS   Itoh,N. and Kavanaugh,M.W.
  TITLE     Human fgf-23 gene and gene expression products
  JOURNAL   Patent: WO 0166596-A 1 13-SEP-2001;
            CHIRON CORPORATION (US) ; Kyoto University (JP)
FEATURES             Location/Qualifiers
     source          1. .756
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BASE COUNT      141 a    251 c    217 g    147 t
ORIGIN

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  Best Local Similarity   72.9%;  Pred. No. 2e-92;
  Matches  551;  Conservative    0;  Mismatches  205;  Indels    0;  Gaps    0;

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Db      1 ATGCTAGGGACCTGCCTTAGACTCCTGGTGGGCGTGCTCTGCACTGTCTGCAGCTTGGGC 60

Qy    207 GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
          ||||||||||||  |   | ||||||  |||| |||||||  ||||||  |||||| |
Db     61 ACTGCTAGAGCCTATCCAGACACTTCCCCATTGCTTGGCTCCAACTGGGGAAGCCTGACC 120

Qy    267 CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
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Db    121 CACCTGTACACGGCTACAGCCAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCAT 180

Qy    327 GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT 386
          || ||||||| | |||||||||||||||||||||||||||||||| | |||||||||| ||
Db    181 GTAGATGGCACCCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACGCC 240

Qy    387 GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
          |||| ||||||||| ||||| |  ||||   |||| | ||| || |||||| ||   |||
Db    241 GGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCCTTTGTATGGATCTCCACGGC 300

Qy    447 AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG 506
          |||||||||||||| |   | |||  ||| ||||| |||| |||||  ||   |||||||
Db    301 AACATTTTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTG 360

Qy    507 GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG 566
          || || || || |||||||||    || |    || |||||| |||||| || |||||||||
Db    361 GAGAATGGCTATGACGTCTACTTGTCGCAGAAGCATCACTACCTGGTGAGCCTGGGCCGC 420

Qy    567 GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
          || ||| |    |||| ||| ||||  ||||| || || | |||||||||||| | ||
Db    421 GCCAAGCGCATTTTCCAGCCGGGCACCAACCCGCCGCCCTTCTCCCAGTTCCTGGCTCGC 480

Qy    627 AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC 686
          ||||||||| |||| ||  | |||||| ||||       |||||||| ||||| || |||
Db    481 AGGAACGAGGTCCCGCTGCTGCACTTCTACACTGTTCGCCCACGGCGCCACACGCGCAGC 540

Qy    687 GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCGGATGACC 746
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Db    541 GCCGAGGACCCACCCGAGCGCGACCCACTGAACGTGCTCAAGCCGCGGCCCCGCGCCACG 600

Qy    747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806
          || |  || |  ||||| || |  ||||| |||||||| |||||      ||||    |||
Db    601 CCTGTGCCTGTATCCTGCTCTCGCGAGCTGCCGAGCGCAGAGGAAGGTGGCCCCGCAGCC 660

Qy    807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACGCTGGGGGAACGGGC 866
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Db    661 AGCGATCCTCTGGGGGTGCTGCGCAGAGGCCGTGGAGATGCTCGCGGGGGCGCGGGAGGC 720

Qy    867 CCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAG 902
           ||||  | || ||||||||  ||| |||| |||||
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Search completed: May 29, 2003, 01:28:07
Job time : 4859 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 84 Seconds
(without alignments)
615.688 Million cell updates/sec

Title: US-09-901-938-2
Perfect score: 1360
Sequence: 1 MLGARLRLWVCALCSVCSMS.....VNTHAGGTGPEGCRPFAKFI 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	978	71.9	251	11	Q8VI82	Q8vi82 rattus norv
2	239	17.6	208	11	Q8VI80	Q8vi80 rattus norv
3	194.5	14.3	227	13	Q9DDN0	Q9ddn0 gallus gall
4	181.5	13.3	245	11	Q8R5L9	Q8r5l9 rattus norv
5	158	11.6	196	13	Q9YH31	Q9yh31 notophthalm
6	157	11.5	124	13	Q90XQ5	Q90xq5 ambystoma m
7	150.5	11.1	111	13	Q90XQ1	Q90xq1 ambystoma m
8	149.5	11.0	218	11	Q8VI81	Q8vi81 rattus norv
9	147.5	10.8	192	11	Q9ERW3	Q9erw3 rattus norv
10	147.5	10.8	245	11	Q8VCY9	Q8vcy9 mus musculu
11	146.5	10.8	208	6	Q95K97	Q95k97 macaca fasc
12	146	10.7	206	13	Q9YGD8	Q9ygd8 oncorhynchu
13	144	10.6	211	11	Q8R4X0	Q8r4x0 rattus norv
14	143.5	10.6	212	13	O42407	O42407 gallus gall
15	143	10.5	201	13	Q8QG59	Q8qg59 ambystoma m
16	142	10.4	191	13	Q9DFC9	Q9dfc9 brachydanio
17	141	10.4	111	13	Q90Y71	Q90y71 xenopus lae
18	140.5	10.3	199	13	Q9IAI3	Q9iai3 gallus gall
19	140.5	10.3	245	13	Q9W6A2	Q9w6a2 gallus gall
20	140	10.3	252	11	O89096	O89096 rattus norv
21	139.5	10.3	208	4	Q96P59	Q96p59 homo sapien
22	139.5	10.3	208	11	Q8R5L5	Q8r5l5 rattus norv
23	137.5	10.1	253	13	Q9IAI5	Q9iai5 gallus gall
24	136.5	10.0	247	11	Q8R5L7	Q8r5l7 rattus norv
25	134	9.9	237	13	Q9IAI6	Q9iai6 gallus gall
26	132.5	9.7	195	11	Q8R5L6	Q8r5l6 rattus norv
27	132	9.7	213	6	Q9N1B9	Q9n1b9 ovis aries
28	132	9.7	302	11	Q9CSX5	Q9csx5 mus musculu
29	130.5	9.6	212	11	Q9EST9	Q9est9 rattus norv
30	130.5	9.6	212	11	Q9ESL9	Q9esl9 mus musculu
31	130	9.6	207	11	Q9ESL8	Q9esl8 mus musculu
32	129.5	9.5	112	13	Q90XP9	Q90xp9 ambystoma m
33	129	9.5	207	11	Q9ERQ5	Q9erq5 mus musculu
34	128	9.4	185	11	Q9ERN5	Q9ern5 rattus norv
35	128	9.4	186	6	Q95L47	Q95l47 mustela vis
36	127	9.3	134	13	Q90XQ3	Q90xq3 ambystoma m
37	127	9.3	170	11	Q60487	Q60487 cavia porce
38	127	9.3	181	11	Q924B4	Q924b4 rattus norv
39	127	9.3	181	13	Q9IAI7	Q9iai7 gallus gall
40	127	9.3	243	13	Q9W6A1	Q9w6a1 gallus gall
41	125.5	9.2	162	11	Q8VI79	Q8vi79 rattus norv
42	124.5	9.2	153	6	Q8SQ73	Q8sq73 canis famil
43	124.5	9.2	181	4	Q8TBG5	Q8tbg5 homo sapien
44	124	9.1	127	4	Q99517	Q99517 homo sapien
45	123.5	9.1	301	5	Q8T8A3	Q8t8a3 ciona savig

ALIGNMENTS

RESULT 1
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ID Q8VI82 PRELIMINARY; PRT; 251 AA.
AC Q8VI82;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibroblast growth factor 23.
GN FGF23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Rattus norvegicus fgf23.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB078777; BAB84108.1; -.
DR InterPro; IPR002209; HB/F_growthfact.
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 251 AA; 27911 MW; 35A229E1B3900593 CRC64;

Query Match 71.9%; Score 978; DB 11; Length 251;
Best Local Similarity 71.7%; Pred. No. 3.9e-86;
Matches 180; Conservative 26; Mismatches 45; Indels 0; Gaps 0;

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Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
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Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Db    121 ENGYDVYLSPKHHYLVSLGRSKRIFQPGTNPPPFSQFLARRNEVPLLHFYTARPRRHTRS 180

Qy    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Db    181 AEDPPERDPLNVLKPRPRATPIPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARRGAGG 240

Qy    241 PEGCRPFAKFI 251

Db    241 TDRCRPFPRFV 251


RESULT 2
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AC   Q8VI80;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 21.
GN   FGF21.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Itoh N.;
RT   "Ruttus norvegicus FGF21.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB078901; BAB84299.1; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
SQ   SEQUENCE   208 AA;  22857 MW;  D232445902CDB8EA CRC64;

  Query Match           17.6%;  Score 239;  DB 11;  Length 208;
  Best Local Similarity   31.2%;  Pred. No. 4.5e-15;
  Matches   67;  Conservative   39;  Mismatches   73;  Indels   36;  Gaps    8;

Qy      8 LWVCALCSVCSMSVLRAYP--NASPLLGSSWGGLI---HLYTATARNS-YHLQIHKNGHV 61

Db     13 LWVCLLLPVFLLGVCEAYPISDSSPLL--QFGGQVRQRYLYTDDDQDTEAHLEIREDGTV 70

Qy     62 DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLE 121

Db     71 VGTAHRSPESLLELKALKPGVIQILGVKASRFLCQQPDGTLYGSPHFDPEACSFRELLLK 130

Qy    122 NGYDVYHSPQYHFLVSL----------GRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFN 170

Db    131 DGYNVYQSEAHGLPLRLPQKDSQDPATRGPVRFLPMPGLPHEPQEQ----PGVLP----- 181

Qy    171 TPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS 205

Db    182 -PEP-------PDVGSSDPLSMVEPLQGRSPSYAS 208


RESULT 3
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ID   Q9DDN0      PRELIMINARY;      PRT;   227 AA.
AC   Q9DDN0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 19.
GN   FGF-19.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20564778; PubMed=11110663;
RA   Ladher R.K., Anakwe K.U., Gurney A.L., Schoenwolf G.C.,
RA   Francis-West P.H.;
RT   "Identification of Synergistic Signals Initiating Inner Ear
RT   Development.";
RL   Science 290:1965-1968(2000).
DR   EMBL; AF315355; AAG39478.1; -.
DR   HSSP; P09038; 1BFG.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ   SEQUENCE   227 AA;  24568 MW;  875D76FBFD09F8E2 CRC64;

  Query Match           14.3%;  Score 194.5;  DB 13;  Length 227;
  Best Local Similarity   29.9%;  Pred. No. 9.7e-11;
  Matches   67;  Conservative   30;  Mismatches  104;  Indels   23;  Gaps    7;

Qy      3 GARLRLWVCALCSVCSMSVLRAYPN-ASPLLGSSWGGLIHLYTATARNSYH------LQI 55

Db     10 GAALALLGIAAAAAAARSL--PLPDVGGPHVNYGWGEPIRLRHLLHRPGKHGLFSCFLRI 67

Qy     56 HKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRF 115

Db     68 GGDGRVDAVGSQSPQSLLEIRAVAVRTVAIKGVQSSRYLCMDEAGRLHGQLSYSIEDCSF 127

Qy    116 QHQTLENGYDVYHSPQYHFLVSLGRAK-RAFLPGMNPPPYSQFLSRRNEIPL-------- 166

Db    128 EEEIRPDGYNVYKSKKYGISVSLSSAKQRQQFKGKDFLPLSHFLPMINTVPVEVTDFGEY 187

Qy    167 -IHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQE 209

Db    188 GDYSQAFEPEVYSSPLETDS-MDPFGI---TSKLSPVKSPSFQK 227


RESULT 4
Q8R5L9
ID   Q8R5L9      PRELIMINARY;      PRT;   245 AA.
AC   Q8R5L9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   FGF3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Itoh N.;
RT   "Rattus norvegicus FGF3 mRNA.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB079262; BAB84564.1; -.
SQ   SEQUENCE   245 AA;  27150 MW;  C9305D307E7D0648 CRC64;

  Query Match           13.3%;  Score 181.5;  DB 11;  Length 245;
  Best Local Similarity   29.0%;  Pred. No. 1.9e-09;
  Matches   62;  Conservative   29;  Mismatches   86;  Indels   37;  Gaps    8;

Qy     42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101

Db     48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy    102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152

Db    105 LYASEHYNAE-CEFVERIHELGYNTYASRLYRTGPSGPGARRQ--PGAQRPWYVSVNGKG 161

Qy    153 -PYSQFLSRRNEIPLIHFNTPIPR-------RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
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Db    162 RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSGQPQAPGEGSQPRQR------ 211

Qy    205 SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
Db    212 --RQKKQSPGDHGKMEHLPTKATTSAQLDT--GG 241


RESULT 5
Q9YH31
ID   Q9YH31      PRELIMINARY;      PRT;   196 AA.
AC   Q9YH31;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative fibroblast growth factor-4.
OS   Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC   Notophthalmus.
OX   NCBI_TaxID=8316;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wei Y.;
RT   "Putative Newt Fibroblast Growth Factor-4.";
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U76998; AAC98812.1; -.
DR   HSSP; P09038; 1BFF.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
SQ   SEQUENCE   196 AA;  22033 MW;  AC4688CD989C6EAF CRC64;

  Query Match             11.6%;  Score 158;  DB 13;  Length 196;
  Best Local Similarity   34.8%;  Pred. No. 2.6e-07;
  Matches   39;  Conservative   16;  Mismatches   41;  Indels   16;  Gaps    3;

Qy     51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
Db     84 FHLQVLPDGRIHGMHSESRYSLLEISPVERGVVCMFGVQSGLFLAMNSKGRLFGSKYFSD 143

Qy    111 ENCRFQHQTLENGYDVYHS----PQYHFLVSLGRAKRA-----------FLP 147
Db    144 E-CKFKEMLLPNNYNAYESWRYPGMYIALSKNGRAKKGNKVSPTMTVTHFLP 194


RESULT 6
Q90XQ5
ID   Q90XQ5      PRELIMINARY;      PRT;   124 AA.
AC   Q90XQ5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 4 (Fragment).
OS   Ambystoma mexicanum (Axolotl).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=8296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21439472; PubMed=11555861;
RA   Christensen R.N., Weinstein M., Tassava R.A.;
RT   "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT   and semi-quantitative RT-PCR expression studies.";
RL   J. Exp. Zool. 290:529-540(2001).
DR   EMBL; AF360984; AAL16957.1; -.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   Pfam; PF00167; FGF; 1.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT   NON_TER       1      1
SQ   SEQUENCE   124 AA;  14161 MW;  919CE10E9F66CEF3 CRC64;

  Query Match             11.5%;  Score 157;  DB 13;  Length 124;
  Best Local Similarity   35.3%;  Pred. No. 1.9e-07;
  Matches   41;  Conservative   18;  Mismatches   47;  Indels   10;  Gaps    4;

Qy     51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
Db     12 FHVQVLPDGRIHGTHNENRYSLLEISPVERGVVSILGVKSALFLAMNNRGKLYGSKQYN- 70

Qy    111 ENCRFQHQTLENGYDVYHSPQYH----FLVSLGRAKRA--FLPGMNPPPYSQFLSR 160
Db     71 EECKFKETLLANNYNAYESRQYPGMYIALSKNGRTKRGNRVSPTMN---VTHFLPR 123


RESULT 7
Q90XQ1
ID   Q90XQ1      PRELIMINARY;      PRT;   111 AA.
AC   Q90XQ1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 4 (Fragment).
OS   Ambystoma maculatum (spotted salamander).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=43114;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21439472; PubMed=11555861;
RA   Christensen R.N., Weinstein M., Tassava R.A.;
RT   "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT   and semi-quantitative RT-PCR expression studies.";
RL   J. Exp. Zool. 290:529-540(2001).
DR   EMBL; AF360988; AAL16961.1; -.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   Pfam; PF00167; FGF; 1.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12607 MW;  4A3A52ED39001057 CRC64;

  Query Match             11.1%;  Score 150.5;  DB 13;  Length 111;
  Best Local Similarity   36.1%;  Pred. No. 6.8e-07;
  Matches   35;  Conservative   16;  Mismatches   41;  Indels    5;  Gaps    2;

Qy     51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
Db     12 FHVQVLPDGKIHGTHNENRYSLLEISPVERGVVSILGVKSALFLAMNNRGKLYGSKQYS- 70

Qy    111 ENCRFQHQTLENGYDVYHSPQYH----FLVSLGRAKR 143
Db     71 EECKFKEPLLANNYNAYESRQYPGMYIALSKNGRTKR 107


RESULT 8
Q8VI81
ID   Q8VI81      PRELIMINARY;      PRT;   218 AA.
AC   Q8VI81;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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DE   Fibroblast growth factor 15.
GN   FGF15.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Itoh N.;
RT   "Rattus norvegicus FGF15.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB078900; BAB84298.1; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ   SEQUENCE   218 AA;  25207 MW;  ED898684B5307C58 CRC64;

  Query Match             11.0%;  Score 149.5;  DB 11;  Length 218;
  Best Local Similarity   26.3%;  Pred. No. 2e-06;
  Matches   51;  Conservative   26;  Mismatches   80;  Indels   37;  Gaps    6;

Qy      30 PLLGSSWGGLIHLYTATARNSY----HLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVI 85
           ||    || :  |    :   |     |:|  :| ||    |   : |  |:    : |
Db      40 PLFLYGWGKITRLQYLYSAGPYVSNCFLRIRSDGSVDCEEDQNERNLLEFRAVALKTIAI 99

Qy      86 TGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAK-RA 144
             | | |||||   | |:|   :  |:| |: :    ||: | | ::|  :   :|| |
Db     100 KDVSSVRYLCMSADGKIYGLIRYSEEDCTFREEMDCLGYNQYRSMKHHLHIIFIKAKPRE 159

Qy     145 FLPGMNPPPYSQFLSRRNEIPLIH--------------FNTPIPRRHTRSAEDDSERDPL 190
           | | |           | ||: |               |: |:        | ||  ||
Db     160 QLQGQKP---------SNFIPIFHRSFFESTDQLRSKMFSLPL--------ESDS-MDPF 201

Qy     191 NVLKPRARMTPAPA 204
           :::    :  :|:
Db     202 RMVEDVDHLVKSPS 215


RESULT 9
Q9ERW3
ID   Q9ERW3      PRELIMINARY;      PRT;   192 AA.
AC   Q9ERW3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 13.
GN   FGF13.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=DORSAL ROOT GANGLION;
RA   Xiao H., Huang Q., Zhang F., Guo C., Chen Z., Han Z., Zhang X.;
RT   "Rattus norvegicus fibroblast growth factor 13.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF271786; AAG15492.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
SQ   SEQUENCE   192 AA;  21604 MW;  7736A3671677B263 CRC64;

  Query Match             10.8%;  Score 147.5;  DB 11;  Length 192;
  Best Local Similarity   25.1%;  Pred. No. 2.6e-06;
  Matches   54;  Conservative   31;  Mismatches   81;  Indels   49;  Gaps   10;

Qy      37 GGLIHLYTATARNSYHLQIHKNGHVDGAPHQ-TIYSALMIRSEDAGFVVITGVMSRRYLC 95
           | :  ||   :|  ||||:  :| :||   : : |:   :       | | || :: ||
Db      15 GIVTKLY---SRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA 71

Qy      96 MDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYS 155
           |:  | :: | :| || |:|:    || |  | |  |       :: | :  |:|
Db      72 MNSEGYLYTSEHFTPE-CKFKESVFENYYVTYSSMIYR----QQQSGRGWYLGLN----- 121

Qy     156 QFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQ-ELPSAE 214
             :  ||        :   | :               || |   | |   :  : ||
Db     122 ----KEGEI--------MKGNHVKKN-----------KPAAHFLPKPLKVAMYKEPSLH 157

Qy     215 D---------NSPMASDPL-GVVRGGRVNTHAGGT 239
           |           :|  |  : ||: ||:  :|   |
Db     158 DLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST 192


RESULT 10
Q8VCY9
ID   Q8VCY9      PRELIMINARY;      PRT;   245 AA.
AC   Q8VCY9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 13.
GN   FGF13.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018238; AAH18238.1; -.
DR   MGD; MGI:109178; Fgf13.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ   SEQUENCE   245 AA;  27587 MW;  5B96D41AC3A3DF78 CRC64;

  Query Match             10.8%;  Score 147.5;  DB 11;  Length 245;
  Best Local Similarity   25.1%;  Pred. No. 3.6e-06;
  Matches   54;  Conservative   31;  Mismatches   81;  Indels   49;  Gaps   10;

Qy      37 GGLIHLYTATARNSYHLQIHKNGHVDGAPHQ-TIYSALMIRSEDAGFVVITGVMSRRYLC 95
           | :  ||   :|  ||||:  :| :||   : : |:   :       | | || :: ||
Db      68 GIVTKLY---SRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA 124

Qy      96 MDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYS 155
           |:  | :: | :| || |:|:    || |  | |  |       :: | :  |:|
Db     125 MNSEGYLYTSEHFTPE-CKFKESVFENYYVTYSSMIYR----QQQSGRGWYLGLN----- 174

Qy     156 QFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQ-ELPSAE 214
             :  ||        :   | :               || |   | |   :  : ||
Db     175 ----KEGEI--------MKGNHVKKN-----------KPAAHFLPKPLKVAMYKEPSLH 210

Qy     215 D---------NSPMASDPL-GVVRGGRVNTHAGGT 239
           |           :|  |  : ||: ||:  :|   |
Db     211 DLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST 245


RESULT 11
Q95K97
ID   Q95K97      PRELIMINARY;      PRT;   208 AA.
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AC   Q95K97;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 23.5 kDa protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MEDULLA OBLOGATA;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB063051; BAB60779.1; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   Pfam; PF00167; FGF; 1.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   208 AA;  23466 MW;  0766A787609B3661 CRC64;

  Query Match             10.8%;  Score 146.5;  DB 6;  Length 208;
  Best Local Similarity   32.0%;  Pred. No. 3.7e-06;
  Matches   39;  Conservative   20;  Mismatches   54;  Indels    9;  Gaps    4;

Qy      51 YHLQIHKNGHVDGAPHQTI-YSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFD 109
           | |:| ||| | |    :   || | | | : | | :  : |  || |: :| ::||  |:
Db      88 YFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFN 147

Qy     110 PENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNE----IP 165
             :|: : :  ||||: | |  :      ||     | |   |   |   |:|     :|
Db     148 -NDCKLKERIEENGYNTYASFNWQ---HNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLP 203

Qy     166 LI 167
           ::
Db     204 MV 205


RESULT 12
Q9YGD8
ID   Q9YGD8       PRELIMINARY;      PRT;   206 AA.
AC   Q9YGD8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 6-related protein.
GN   FGF6.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99096461; PubMed=9878802;
RA   Rescan P.Y.;
RT   "Identification of a fibroblast growth factor 6 (FGF6) in a non-
RT   mammalian vertebrate: Continuous expression of FGF6 accompanies muscle
RT   fiber hyperplasia.";
RL   Biochim. Biophys. Acta 1443:305-314(1998).
DR   EMBL; Y16850; CAA76422.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
SQ   SEQUENCE   206 AA;  23375 MW;  BB883328F17EB6E4 CRC64;

  Query Match             10.7%;  Score 146;  DB 13;  Length 206;
  Best Local Similarity   31.2%;  Pred. No. 4e-06;
  Matches   35;  Conservative   20;  Mismatches   41;  Indels   16;  Gaps    3;

Qy      51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
           :|||:  :| ::|  ::  || : | : : | | : || |  :: |: || ::|:  |
Db      94 FHLQVLPDGRINGVHNENQYSLIEISTVERGVVSLYGVRSELFVAMNSRGRLYGTTVFHD 153

Qy     111 ENCRFQHQTLENGYDVYHSPQYH----FLVSLGRAKRA----------FLP 147
           | |:|:   | | |: | |  |       |   || ||           |||
Db     154 E-CKFRESMLPNNYNAYESSVYRGSYIALNKHGRLKRGKKATTAMTVTHFLP 204


RESULT 13
Q8R4X0
ID   Q8R4X0       PRELIMINARY;      PRT;   211 AA.
AC   Q8R4X0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor-like factor-4D (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu C., Dib-Hajj S.D., Waxman S.G.;
RT   "Fibroblast growth factor homologous factor-4D.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF348523; AAL83904.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   211 AA;  23346 MW;  046C18019C63EBA3 CRC64;

  Query Match             10.6%;  Score 144;  DB 11;  Length 211;
  Best Local Similarity   24.7%;  Pred. No. 6.5e-06;
  Matches   54;  Conservative   39;  Mismatches   78;  Indels   48;  Gaps   11;

Qy       9 WVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVDG----A 64
           ||  |  :|  |: :   | :|       | :  ||     |  |:||:| :| :||    :
Db      11 WV--LQCLCGKSLKK---NKNPTDPQLKGIVTRLY---CRQGYYLQMHPDGALDGTKDDS 62

Qy      65 PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY 124
           : |::: : :       | | || :  |: |:  | :: |  | || |:|:    || |
Db      63 TNSTLFNLIPV---GLRVVAIQGVKTGLYIAMNGEGYLYPSELFTPE-CKFKESVFENYY 118

Qy     125 DVYHSPQYHFLVSLGRAKRAFLPGMN------------PPPYSQFLSRRNEIPLIHFNT 171
           :| |  |        : ||:  |:|               | : || :  |: :  :
Db     119 VIYSSMLYR----QQESGRAWFLGLNKEGQVMKGNRVKKTKPAAHFLPKPLEVAM--YRE 172

Qy     172 PIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQEL 210
           |       |  |  |       |:| :||: :: :  :
Db     173 P-------SLHDVGE------TVPKAGVTPSKSTSASAI 198


RESULT 14
O42407
ID   O42407       PRELIMINARY;      PRT;   212 AA.
AC   O42407;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 10.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97330690; PubMed=9187149;
RA   Ohuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
RA   Yoshioka H., Kuwana T., Nohno T., Yamasaki M., Itoh N., Noji S.;
RT   "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
RT   of the chick limb bud through interaction with FGF8, an apical
RT   ectodermal factor.";
RL   Development 124:2235-2244(1997).
DR   EMBL; D86333; BAA24945.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   Pfam; PF00167; FGF; 1.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
SQ   SEQUENCE   212 AA;  23631 MW;  AB4C0B32C72A0D90 CRC64;

  Query Match             10.6%;  Score 143.5;  DB 13;  Length 212;
  Best Local Similarity   31.9%;  Pred. No. 7.3e-06;
  Matches   38;  Conservative   19;  Mismatches   41;  Indels   21;  Gaps    5;

Qy      49 NSYHLQIHKNGHVDGAPHQTI-YSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHY 107
           | | |:| |||| | |    :   :| | | | : | | :  : |  || |: :| ::||
Db      90 NKYFLKIEKNGKVSGTKKENCPFSILEITSVEIGVVAVKSIKSNYYLAMNKKGKVYGSKE 149

Qy     108 FDPENCRFQHQTLENGYDVY------HSPQYHFLVSLGR--AKRA-----------FLP 147
           |:  :|: : :  ||||: |      |: :  |:   ||   ||            |||
Db     150 FN-SDCKLKERIEENGYNTYASLNWKHNGRQMFVALNGRGATKRGQKTRRKNTSAHFLP 207


RESULT 15
Q8QG59
ID   Q8QG59      PRELIMINARY;      PRT;   201 AA.
AC   Q8QG59;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibroblast growth factor 10.
OS   Ambystoma mexicanum (Axolotl).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=8296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21826199; PubMed=11836784;
RA   Christensen R.N., Weinstein M., Tassava R.A.;
RT   "Expression of fibroblast growth factors 4, 8, and 10 in limbs,
RT   flanks, and blastemas of Ambystoma.";
RL   Dev. Dyn. 223:193-203(2002).
DR   EMBL; AY034453; AAK59700.1; -.
SQ   SEQUENCE   201 AA;  22994 MW;  89EA1E61806A6F57 CRC64;

  Query Match             10.5%;  Score 143;  DB 13;  Length 201;
  Best Local Similarity   27.5%;  Pred. No. 7.6e-06;
  Matches   47;  Conservative   25;  Mismatches   79;  Indels   20;  Gaps    6;

Qy       6 LRLWVCALCSVC-----SMSVLRAYPNASPLLG------SSWGGLIHLYTATARNSYHLQ 54
           | |||  |   |      |       :: |::|          | : |       :| |:
Db      21 LLLWVSCLSVTCHDLARDMLSPEVANSSVPVVGRQVRSYKHLEGDVRLRRLLCVTNYFLK 80

Qy      55 IHKNGHVDGAPH-QTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC 113
           |  :| | |      || : | | | | | : || |  || |: :| ::||  |  : |
Db      81 IDADGKVSGTTKVDCPYSVMEITSVDVGIVAVKGVYSNYYLAMNEKGRVYGSREFTTD-C 139

Qy     114 RFQHQTLENGYDVYHSPQYHFLVSLGRAKRAF--LPGMNPPPYSQFLSRRN 162
           : : :  || |: | | ::       : :: |  | |   |   |   |:|
Db     140 KLKERMEENKYNTYASYKWRH-----KQRQMFVALNGKGTPKRGQKTKRKN 185


Search completed: May 23, 2003, 07:45:45
Job time : 86 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 25 Seconds
(without alignments)
416.422 Million cell updates/sec

Title: US-09-901-938-2
Perfect score: 1360
Sequence: 1 MLGARLRLWVCALCSVCSMS.....VNTHAGGTGPEGCRPFAKFI 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1360	100.0	251	1	FGFN_HUMAN	Q9gzv9 homo sapien
2	961	70.7	251	1	FGFN_MOUSE	Q9epc2 mus musculu
3	241	17.7	210	1	FGFL_MOUSE	Q9jjn1 mus musculu
4	222.5	16.4	209	1	FGFL_HUMAN	Q9nsa1 homo sapien
5	207	15.2	216	1	FGFJ_HUMAN	O95750 homo sapien
6	182.5	13.4	245	1	FGF3_MOUSE	P05524 mus musculu
7	180.5	13.3	239	1	FGF3_HUMAN	P11487 homo sapien
8	178.5	13.1	237	1	FGF3_XENLA	P36386 xenopus lae
9	176.5	13.0	266	1	FGF5_RAT	P48807 rattus norv
10	171	12.6	264	1	FGF5_MOUSE	P15656 mus musculu
11	168.5	12.4	268	1	FGF5_HUMAN	P12034 homo sapien
12	167	12.3	220	1	FGF3_CHICK	P48801 gallus gall
13	159.5	11.7	256	1	FGF3_BRARE	P48802 brachydanio
14	155	11.4	192	1	FGFB_XENLA	P48806 xenopus lae
15	151	11.1	187	1	FGFA_XENLA	P48805 xenopus lae
16	147.5	10.8	245	1	FGFD_MOUSE	P70377 mus musculu
17	146.5	10.8	194	1	FGF4_CHICK	P48804 gallus gall
18	146.5	10.8	208	1	FGFA_HUMAN	O15520 homo sapien
19	146.5	10.8	215	1	FGFA_RAT	P70492 rattus norv
20	145.5	10.7	209	1	FGFA_MOUSE	O35565 mus musculu
21	144.5	10.6	245	1	FGFD_HUMAN	Q92913 homo sapien
22	142	10.4	206	1	FGF4_BOVIN	P48803 bos taurus
23	141.5	10.4	208	1	FGF6_HUMAN	P10767 homo sapien
24	141.5	10.4	218	1	FGFF_MOUSE	O35622 mus musculu
25	138.5	10.2	208	1	FGF6_MOUSE	P21658 mus musculu
26	136.5	10.0	247	1	FGFE_MOUSE	P70379 mus musculu
27	135	9.9	247	1	FGFE_HUMAN	Q92915 homo sapien
28	132.5	9.7	211	1	FGFK_HUMAN	Q9np95 homo sapien
29	132	9.7	207	1	FGFG_RAT	O54769 rattus norv
30	131.5	9.7	206	1	FGF4_HUMAN	P08620 homo sapien
31	131	9.6	202	1	FGF4_MOUSE	P11403 mus musculu
32	129	9.5	207	1	FGFG_HUMAN	O43320 homo sapien
33	128	9.4	194	1	FGF7_CANFA	P79150 canis famil
34	128	9.4	194	1	FGF7_MOUSE	P36363 mus musculu
35	127	9.3	194	1	FGF7_PIG	Q9n198 sus scrofa
36	127	9.3	194	1	FGF7_SHEEP	P48808 ovis aries
37	127	9.3	243	1	FGFC_HUMAN	Q92912 homo sapien
38	126	9.3	194	1	FGF7_HUMAN	P21781 homo sapien
39	124.5	9.2	162	1	FGFM_MOUSE	Q9ess2 mus musculu
40	118.5	8.7	170	1	FGFM_HUMAN	Q9hct0 homo sapien
41	118	8.7	208	1	FGF9_HUMAN	P31371 homo sapien
42	118	8.7	208	1	FGF9_MOUSE	P54130 mus musculu
43	118	8.7	208	1	FGF9_RAT	P36364 rattus norv
44	117	8.6	154	1	FGF2_RAT	P13109 rattus norv
45	116.5	8.6	154	1	FGF2_MOUSE	P15655 mus musculu

ALIGNMENTS

RESULT 1
FGFN_HUMAN
ID FGFN_HUMAN STANDARD; PRT; 251 AA.
AC Q9GZV9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23) (Tumor-derived
DE hypophosphatemia inducing factor).
GN FGF23 OR HYPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20490027; PubMed=11032749;
RA Yamashita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23,
RT preferentially expressed in the ventrolateral thalamic nucleus of the
RT brain.";
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A., VARIANTS ADHR Q-176; Q-179 AND W-179, AND
RP VARIANTS M-239.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with
RT mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11344269;
RA Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takeda S.,
RA Takeuchi Y., Fujita T., Fukumoto S., Yamashita T.;
RT "Cloning and characterization of FGF23 as a causative factor of
RT tumor-induced osteomalacia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- DISEASE: DEFECTS IN FGF23 ARE THE CAUSE OF AUTOSOMAL DOMINANT
CC HYPOPHOSPHATAEMIC RICKETS (ADHR). ADHR IS CHARACTERIZED BY LOW
CC SERUM PHOSPHORUS CONCENTRATIONS, RICKETS, OSTEOMALACIA, LEG
CC DEFORMITIES, SHORT STATURE, BONE PAIN AND DENTAL ABSCESSES.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC ----------

CC ----------
DR EMBL; AB037973; BAB13477.1; -.
DR EMBL; AF263537; AAG09917.1; -.

```
DR   EMBL; AB047858; BAB55889.1; -.
DR   HSSP; P03968; 1AFC.
DR   Genew; HGNC:3680; FGF23.
DR   MIM; 605380; -.
DR   MIM; 193100; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW   Growth factor; Signal; Disease mutation; Polymorphism.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    251       FIBROBLAST GROWTH FACTOR-23.
FT   VARIANT     176    176       R -> Q (IN ADHR).
FT                                /FTId=VAR_010717.
FT   VARIANT     179    179       R -> Q (IN ADHR).
FT                                /FTId=VAR_010719.
FT   VARIANT     179    179       R -> W (IN ADHR).
FT                                /FTId=VAR_010718.
FT   VARIANT     239    239       T -> M.
FT                                /FTId=VAR_010720.
SQ   SEQUENCE   251 AA;  27954 MW;  6093BD0CC50C2489 CRC64;

  Query Match             100.0%;  Score 1360;  DB 1;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 4e-116;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           ||||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 2
FGFN_MOUSE
ID   FGFN_MOUSE     STANDARD;      PRT;   251 AA.
AC   Q9EPC2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-23 precursor (FGF-23).
GN   FGF23.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20490027; PubMed=11032749;
RA   Yamashita T., Yoshioka M., Itoh N.;
RT   "Identification of a novel fibroblast growth factor, FGF-23,
RT   preferentially expressed in the ventrolateral thalamic nucleus of the
RT   brain.";
RL   Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Embryo;
RX   MEDLINE=20517346; PubMed=11062477;
RA   White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA   Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT   "Autosomal dominant hypophosphataemic rickets is associated with
RT   mutations in FGF23.";
RL   Nat. Genet. 26:345-348(2000).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE BRAIN AND THYMUS AT
CC       LOW LEVELS. IN BRAIN; PREFERENTIALLY EXPRESSED IN THE
CC       VENTROLATERAL THALAMIC NUCLEUS.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB037889; BAB13478.1; -.
DR   EMBL; AF263536; AAG09916.1; -.
DR   HSSP; P03968; 1BAR.
DR   MGD; MGI:1891427; Fgf23.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW   Growth factor; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    251       FIBROBLAST GROWTH FACTOR-23.
SQ   SEQUENCE   251 AA;  27757 MW;  110C1F2C735DC360 CRC64;

  Query Match             70.7%;  Score 961;  DB 1;  Length 251;
  Best Local Similarity   70.5%;  Pred. No. 5.7e-80;
  Matches  177;  Conservative   25;  Mismatches   49;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           |||  ||| |  ||:|||:   ||||: |||||:|| | |||||||| |||||||::||
Db       1 MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATARTSYHLQIHRDGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           |||  |||||||||| ||||| ||||| |:||:|||| ||||||  :| ||||:|:  ||
Db      61 VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHGNIFGSLHFSPENCKFRQWTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||| | ::|:|||||||| | || ||||:||||:||||:||:|| |  |||||||
Db     121 ENGYDVYLSQKHHYLVSLGRAKRIFQPGTNPPPFSQFLARRNEVPLLHFYTVRPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           |||  |||||||||||| | || | |||:||||||:  | |||||||:| || :   |  |
Db     181 AEDPPERDPLNVLKPRPRATPVPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARGGAGG 240

Qy     241 PEGCRPFAKFI 251
           : |||| :|:
Db     241 ADRCRPFPRFV 251


RESULT 3
FGFL_MOUSE
ID   FGFL_MOUSE     STANDARD;      PRT;   210 AA.
AC   Q9JJN1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-21 precursor (FGF-21).
GN   FGF21.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20461777; PubMed=10858549;
RA   Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT   "Identification of a novel FGF, FGF-21, preferentially expressed in
RT   the liver.";
RL   Biochim. Biophys. Acta 1492:203-206(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN THE LIVER, ALSO
CC       EXPRESSED IN THE THYMUS AT LOWER LEVELS.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB025718; BAA99416.1; -.
DR   EMBL; AK007574; BAB25115.1; -.
DR   HSSP; P03968; 1BAR.
DR   MGD; MGI:1861377; Fgf21.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW   Growth factor; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    210       FIBROBLAST GROWTH FACTOR-21.
SQ   SEQUENCE   210 AA;  23237 MW;  AE02AABA6477E6F0 CRC64;

  Query Match           17.7%;  Score 241;  DB 1;  Length 210;
  Best Local Similarity  32.3%;  Pred. No. 7.9e-15;
  Matches   71;  Conservative   38;  Mismatches   71;  Indels   40;  Gaps    8;

Qy       6 LRLWVCALCSVCSMSVLRAY--PNASPLLGSSWGGLI---HLYTATARNS-YHLQIHKNG 59
           | |||  | :|  : | :||  |::||||   :|| :   :|||   :::  ||:| ::|
Db      11 LGLWVRLLLAVFLLGVYQAYPIPDSSPLL--QFGGQVRQRYLYTDDDQDTEAHLEIREDG 68

Qy      60 HVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQT 119
             | ||  |::   | |  :::   | : | || : |:||    | ::|| :|||| | |:
Db      69 TVVGAAHRSPESLLELKALKPGVIQILGVKASRFLCQQPDGALYGSPHFDPEACSFRELL 128

Qy     120 LENGYDVYHSPQYHFL-------------VSLGRAKRAFLPGMNPPPYSQFLSRRNEIP 165
           ||:||:|| | : | |                | |  :   :||:   |  |
Db     129 LEDGYNVYQS-EAHGLPLRLPQKDSPNQDATSWGPVRFLPMPGLLHEPQDQ--------- 178

Qy     166 LIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS 205
             |  | |        |    |||::::|    :|: ||
Db     179 -AGFLPPEP-------PDVGSSDPLSMVEPLQGRSPSYAS 210


RESULT 4
FGFL_HUMAN
ID   FGFL_HUMAN     STANDARD;      PRT;   209 AA.
AC   Q9NSA1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-21 precursor (FGF-21).
GN   FGF21.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20461777; PubMed=10858549;
RA   Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT   "Identification of a novel FGF, FGF-21, preferentially expressed in
RT   the liver.";
RL   Biochim. Biophys. Acta 1492:203-206(2000).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB021975; BAA99415.1; -.
DR   HSSP; P03968; 1BAR.
DR   Genew; HGNC:3678; FGF21.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW   Growth factor; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    209       FIBROBLAST GROWTH FACTOR-21.
SQ   SEQUENCE   209 AA;  22300 MW;  27925C52A0023823 CRC64;

  Query Match           16.4%;  Score 222.5;  DB 1;  Length 209;
  Best Local Similarity  30.8%;  Pred. No. 3.7e-13;
  Matches   68;  Conservative   36;  Mismatches   70;  Indels   47;  Gaps    9;

Qy       8 LWVCALCSVCSMSVLRAY--PNASPLLGSSWGGLI---HLYTATARNS-YHLQIHKNGHV 61
           |||  |  :  :  :|:  |::||||   :|| :   :|||  |: :  ||:| ::| |
Db      13 LWVSVLAGLL-LGACQAHPIPDSSPLL--QFGGQVRQRYLYTDDAQQTEAHLEIREDGTV 69

Qy      62 DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLE 121
           ||  |: | | :::   | : | || : |:||    | ::|| :|||| | |:   ||
Db      70 GGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLE 129

Qy     122 NGYDVYHSPQYHFLVSL-------------GRAKRAFLPGMNP----PPYSQFLSRRNEI 164
           :||:|| |  :   : |               | |:   |||: |    ||
Db     130 DGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP---------- 178

Qy     165 PLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS 205
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                 | |         |    |||::: |    :|: ||
Db    179 ---GILAPQP-------PDVGSSDPLSMVGPSQGRSPSYAS 209


RESULT 5
FGFJ_HUMAN
ID   FGFJ_HUMAN    STANDARD;      PRT;   216 AA.
AC   O95750;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-19 precursor (FGF-19).
GN   FGF19.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99132028; PubMed=9931477;
RA   Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
RT   "Structure and expression of a novel human FGF, FGF-19, expressed in
RT   the fetal brain.";
RL   Biochim. Biophys. Acta 1444:148-151(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,
RA   Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A.,
RA   Gurney A.L.;
RT   "FGF-19, a novel fibroblast growth factor with unique specificity for
RT   FGFR4.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN BRAIN DEVELOPMENT DURING
CC       EMBRYOGENESIS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN FETAL BRAIN.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AB018122; BAA75500.1; -.
DR   EMBL; AF110400; AAD45973.1; -.
DR   EMBL; BC017664; AAH17664.1; -.
DR   HSSP; P09038; 1BFG.
DR   Genew; HGNC:3675; FGF19.
DR   MIM; 603891; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    216       FIBROBLAST GROWTH FACTOR-19.
SQ   SEQUENCE   216 AA;  24002 MW;  E0BCBC9C220F9832 CRC64;

  Query Match             15.2%;  Score 207;  DB 1;  Length 216;
  Best Local Similarity   28.8%;  Pred. No. 9.9e-12;
  Matches   67;  Conservative   31;  Mismatches   91;  Indels   44;  Gaps    6;
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Qy       6 LRLWVCALCSVCSMSVLRAYPNASPLLGSSWGG---LIHLYTATAR--NSYHLQIHKNGH 60
           : :|: |   :        |: :| | :   ||    | ||||:     :|  |:|  :|
Db       8 VHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRIRADGV 67

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           || |  |: :| | |::     | | || | |||||   | : |   :  |:| |: :
Db      68 VDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEIR 127

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           :||:|| | ::   |||  ||:            |    |  :|| ||   :|
Db     128 PDGYNVYRSEKHRLPVSLSSAKQ----------RQLYKNRGFLPLSHFLPMLP------ 170

Qy     181 AEDDSERDPLNVLKPRARMTP-APASCSQELPSAEDNSPM---ASDPLGVVRG 229
                           | |  |      | |   :||:   : || |:| |
Db     171 -----------------MVPEEPEDLRGHLESDMFSSPLETDSMDPFGLVTG 205


RESULT 6
FGF3_MOUSE
ID   FGF3_MOUSE     STANDARD;      PRT;   245 AA.
AC   P05524;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE   (FGF-3) (HBGF-3).
GN   FGF3 OR FGF-3 OR INT-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86247582; PubMed=3013624;
RA   Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT   "Sequence, topography and protein coding potential of mouse int-2: a
RT   putative oncogene activated by mouse mammary tumour virus.";
RL   EMBO J. 5:919-924(1986).
RN   [2]
RP   SEQUENCE OF 1-73 FROM N.A.
RX   MEDLINE=88296404; PubMed=2841106;
RA   Smith R., Peters G., Dickson C.;
RT   "Multiple RNAs expressed from the int-2 gene in mouse embryonal
RT   carcinoma cell lines encode a protein with homology to fibroblast
RT   growth factors.";
RL   EMBO J. 7:1013-1022(1988).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=91193291; PubMed=1964688;
RA   Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA   Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT   "Characterization of int-2: a member of the fibroblast growth factor
RT   family.";
RL   J. Cell Sci. Suppl. 13:87-96(1990).
CC   -!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC   -!- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Y00848; CAA68767.1; -.
DR   PIR; A23930; TVMST2.
DR   HSSP; P09038; 1BFG.
DR   MGD; MGI:95517; Fgf3.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
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DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    245       INT-2 PROTO-ONCOGENE PROTEIN.
FT   CARBOHYD     65     65       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   245 AA;  27214 MW;  70D94FD6A7837C79 CRC64;

  Query Match             13.4%;  Score 182.5;  DB 1;  Length 245;
  Best Local Similarity   29.4%;  Pred. No. 1.9e-09;
  Matches   63;  Conservative   26;  Mismatches   88;  Indels   37;  Gaps    8;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152
           :: | ::: | | |   :  | ||: | |   |    |  |:|   ||   |
Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNEIPLIHFNTPIPR-------RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
            |   | :|| :   :     :||           | :    | |    :|| |
Db     162 RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR------ 211

Qy     205 SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
           |:  |  |:  | : |          | ||
Db     212 --RQKKQSPGDHGKM--ETLSTRATPSTQLHTGG 241


RESULT 7
FGF3_HUMAN
ID   FGF3_HUMAN     STANDARD;      PRT;   239 AA.
AC   P11487;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE   (FGF-3) (HBGF-3).
GN   FGF3 OR INT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=89239468; PubMed=2470007;
RA   Brooks S., Smith R., Casey G., Dickson C., Peters G.;
RT   "Sequence organization of the human int-2 gene and its expression in
RT   teratocarcinoma cells.";
RL   Oncogene 4:429-436(1989).
CC   -!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X14445; CAA32615.1; -.
DR   PIR; S04742; S04742.
DR   HSSP; P31371; 1G82.
DR   Genew; HGNC:3681; FGF3.
DR   MIM; 164950; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    239       INT-2 PROTO-ONCOGENE PROTEIN.
FT   CARBOHYD     65     65       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   239 AA;  26886 MW;  8DBEF17D2B2E3C63 CRC64;

  Query Match             13.3%;  Score 180.5;  DB 1;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 2.8e-09;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |          |:| :   :|   |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
           | :|| :   :     :  |     |  :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 8
FGF3_XENLA
ID   FGF3_XENLA     STANDARD;      PRT;   237 AA.
AC   P36386;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3) (INT-2).
GN   FGF3.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=94038898; PubMed=8223431;
RA   Kiefer P., Mathieu M., Close J.M., Peters G., Dickson C.;
RT   "FGF3 from Xenopus laevis.";
RL   EMBO J. 12:4159-4168(1993).
RN   [2]
RP   SEQUENCE OF 39-137 FROM N.A.
RC   TISSUE=Neurula;
RX   MEDLINE=93048831; PubMed=1425349;
RA   Tannahill D., Isaacs H.V., Close M.J., Peters G., Slack J.M.W.;
RT   "Developmental expression of the Xenopus int-2 (FGF-3) gene:
RT   activation by mesodermal and neural induction.";
RL   Development 115:695-702(1992).
CC   -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; Z25539; CAA80987.1; -.
DR   EMBL; X65237; CAA46341.1; -.
DR   PIR; S39582; S39582.
DR   PIR; S25713; S25713.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
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DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Mitogen; Signal; Glycoprotein.
FT   SIGNAL        1     21
FT   CHAIN        22    237       FIBROBLAST GROWTH FACTOR-3.
FT   CARBOHYD     83     83       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   237 AA;  26984 MW;  EDD31B0893567A2D CRC64;

  Query Match             13.1%;  Score 178.5;  DB 1;  Length 237;
  Best Local Similarity   32.2%;  Pred. No. 4.3e-09;
  Matches   55;  Conservative   26;  Mismatches   63;  Indels   27;  Gaps    8;

Qy      42 LYTATARNSYHLQIHKNGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRG 100
           || ||    |||||| || ::|    :::| | | : | | | | |: | ||| |: ||
Db      66 LYCAT---KYHLQIHLNGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLAMNQRG 122

Qy     101 NIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVS------LGRAKRAFLPGMNPP-- 152
           :: |  ::|| | |  :  | ||: | |  | : |         |:| :   :|
Db     123 RLYASETYNPE-CEFVERIHELGYNTYASRLYRTVPSGAGTKRKASAERLWYVSINGKGR 181

Qy     153 PYSQFLSRRNE-----IPLIHFN---TPIPRRHTRSAEDDSERDPLNVLKP 195
           |   | :|| :     :| :  |     :   || :   :|      :|||
Db     182 PRRGFKTRRTQKSSLFLPRVLDNKDHDAVRLFHTNAVYRES------ILKP 226


RESULT 9
FGF5_RAT
ID   FGF5_RAT       STANDARD;      PRT;   266 AA.
AC   P48807; Q63402;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
GN   FGF5 OR FGF-5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC   STRAIN=Wistar;
RX   MEDLINE=96201703; PubMed=8611621;
RA   Hattori Y., Yamasaki M., Itoh N.;
RT   "The rat FGF-5 mRNA variant generated by alternative splicing encodes
RT   a novel truncated form of FGF-5.";
RL   Biochim. Biophys. Acta 1306:31-33(1996).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D64085; BAA10966.1; -.
DR   EMBL; D64086; BAA10967.1; -.
DR   HSSP; P09038; 1BFG.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    266       FIBROBLAST GROWTH FACTOR-5.
FT   DOMAIN       54     59       POLY-SER.
FT   CARBOHYD    108    108       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    118    121       ILEI -> QIYR (IN SHORT ISOFORM).
FT   VARSPLIC    122    266       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   266 AA;  29264 MW;  95B0A0CA7C0A200C CRC64;

  Query Match             13.0%;  Score 176.5;  DB 1;  Length 266;
  Best Local Similarity   28.2%;  Pred. No. 7.5e-09;
  Matches   58;  Conservative   34;  Mismatches   75;  Indels   39;  Gaps    8;

Qy      28 ASPLLGSSWGGLIH---LYTATARNS----------YHLQIHKNGHVDGAPHQTIYSALM 74
           |||  ||    |  |    :: : | :          :||||: :| |:|:   :: | |
Db      63 ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILE 120

Qy      75 IRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS----- 129
           | :   | | | || | ::| |  :| :  |  |  ::|:|: :  || |: | |
Db     121 IFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQENSYNTYASAIHRT 179

Qy     130 -----PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHFNTPIPRRHTRSA 181
                |  |   |:|||   | : |   |  || |  ::| | : |  :| :
Db     180 EKTGREWYVALNKRGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEK----- 234

Qy     182 EDDSERDPLNVLKPRARMTPAPASCS 207
               : |    ||:  ::|:  | |
Db     235 -----KKPPRPWKPKVPLSPSRRSPS 255


RESULT 10
FGF5_MOUSE
ID   FGF5_MOUSE     STANDARD;      PRT;   264 AA.
AC   P15656; O88825;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
GN   FGF5 OR FGF-5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=90201563; PubMed=2318343;
RA   Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
RT   "Isolation of cDNAs encoding four mouse FGF family members and
RT   characterization of their expression patterns during embryogenesis.";
RL   Dev. Biol. 138:454-463(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RC   STRAIN=C57BL/6;
RX   MEDLINE=91045929; PubMed=1700424;
RA   Haub O., Drucker B., Goldfarb M.;
RT   "Expression of the murine fibroblast growth factor 5 gene in the
RT   adult central nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
RN   [3]
RP   SEQUENCE FROM N.A. (SHORT ISOFORM).
RA   Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
RA   Imamura T.;
RT   "An alternatively-spliced FGF-5 mRNA is abundant in brain and
RT   translates into a partial agonist/antagonist for FGF-5 neurotrophic
RT   activity.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   ------------------------------------------------------------------------
DR   EMBL; M30643; AAA96698.1; -.
DR   EMBL; M37823; AAB02660.1; -.
DR   EMBL; M37821; AAB02660.1; JOINED.
DR   EMBL; M37822; AAB02660.1; JOINED.
DR   EMBL; M37821; AAB02659.1; ALT_SEQ.
DR   EMBL; AB016516; BAA33737.1; -.
DR   PIR; A36207; A36207.
DR   PIR; B37360; B37360.
DR   HSSP; P09038; 1BFG.
DR   MGD; MGI:95519; Fgf5.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    264       FIBROBLAST GROWTH FACTOR-5.
FT   DOMAIN       53     59       POLY-SER.
FT   CARBOHYD    108    108       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    118    121       ILEI -> QIYG (IN SHORT ISOFORM).
FT   VARSPLIC    122    264       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   264 AA;  29103 MW;  F6A9C8153EE923D1 CRC64;

  Query Match           12.6%;  Score 171;  DB 1;  Length 264;
  Best Local Similarity   27.9%;  Pred. No. 2.3e-08;
  Matches   57;  Conservative   35;  Mismatches   72;  Indels   40;  Gaps    9;

Qy      28 ASPLLGSSWGGLIH---LYTATARNS----------YHLQIHKNGHVDGAPHQTIYSALM 74
           |||  ||    |  |    :: : | :          :||||: :| |:|:   :: | |
Db      63 ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILE 120

Qy      75 IRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS----- 129
           | :   | | | || | ::| |  :| :  |  |  ::|:|: :  || |: | |
Db     121 IFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQENSYNTYASAIHRT 179

Qy     130 -----PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHFNTPIPRRHTRSA 181
                |  |   |:|||   | : |   |  || |  ::| | : |   :|
Db     180 EKTGREWYVALNKRGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVP------- 232

Qy     182 EDDSERDPLNVLKP--RARMTPAP 203
             : :: |:    |  : | :|:|
Db     233 --EKKKPPVKPKVPLSQPRRSPSP 254


RESULT 11
FGF5_HUMAN
ID   FGF5_HUMAN     STANDARD;      PRT;   268 AA.
AC   P12034; O75846;
DT   01-OCT-1989 (Rel. 12, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5) (Smag-82).
GN   FGF5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RC   TISSUE=Brain stem;
RX   MEDLINE=91045929; PubMed=1700424;
RA   Haub O., Drucker B., Goldfarb M.;
RT   "Expression of the murine fibroblast growth factor 5 gene in the
RT   adult central nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=89096942; PubMed=3211147;
RA   Zhan X., Bates B., Hu X., Goldfarb M.;
RT   "The human FGF-5 oncogene encodes a novel protein related to
RT   fibroblast growth factors.";
RL   Mol. Cell. Biol. 8:3487-3495(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (SHORT ISOFORM).
RA   Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
RA   Imamura T.;
RT   "An alternatively-spliced FGF-5 mRNA is abundant in brain and
RT   translates into a partial agonist/antagonist for FGF-5 neurotrophic
RT   activity.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (SHORT ISOFORM).
RC   TISSUE=Umbilical artery;
RX   MEDLINE=20379035; PubMed=10823842;
RA   de Vries C.J.M., van Achterberg T.A.E., Horrevoets A.J.G.,
RA   ten Cate J.W., Pannekoek H.;
RT   "Differential display identification of 40 genes with altered
RT   expression in activated human smooth muscle cells. Local expression
RT   in atherosclerotic lesions of smags, smooth muscle
RT   activation-specific genes.";
RL   J. Biol. Chem. 275:23939-23947(2000).
CC   -!- FUNCTION: THIS ONCOGENE IS EXPRESSED IN NEONATAL BRAIN. FGF-5 CAN
CC       TRANSFORM NIH 3T3 CELLS.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   ------------------------------------------------------------------------
DR   EMBL; M37825; AAB06463.1; -.
DR   EMBL; M23536; AAB60699.1; -.
DR   EMBL; M23534; AAB60699.1; JOINED.
DR   EMBL; M23535; AAB60699.1; JOINED.
DR   EMBL; M23534; AAB60698.1; ALT_SEQ.
DR   EMBL; AB016517; BAA33738.1; -.
DR   EMBL; AF171928; AAF89742.1; -.
DR   PIR; A31194; TVHUF5.
DR   HSSP; P09038; 1BFG.
DR   Genew; HGNC:3683; FGF5.
DR   MIM; 165190; -.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    268       FIBROBLAST GROWTH FACTOR-5.
FT   DOMAIN       49     52       POLY-SER.
FT   DOMAIN       55     62       POLY-SER.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    120    123       VLEI -> QVHR (IN SHORT ISOFORM).
FT   VARSPLIC    124    268       MISSING (IN SHORT ISOFORM).
FT   CONFLICT     42     42       R -> I (IN REF. 1).
FT   CONFLICT     83     86       PSGR -> LGA (IN REF. 2).
SQ   SEQUENCE   268 AA;  29526 MW;  08F4268B26781E9D CRC64;

  Query Match           12.4%;  Score 168.5;  DB 1;  Length 268;
  Best Local Similarity   29.8%;  Pred. No. 4e-08;
  Matches   56;  Conservative   29;  Mismatches   74;  Indels   29;  Gaps    7;

Qy      15 SVCSMSVLRAYPNASPLLGSSWGGL---IHLYTATARNS----------YHLQIHKNGHV 61
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Db      52 SAMSSSSASSSPAAS--LGSQGSGLEQSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKV 109

Qy      62 DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLE 121

Db     110 NGSHEANMLSVLEIFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQE 168

Qy     122 NGYDVYHS----------PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIH 168

Db     169 NSYNTYASAIHRTEKTGREWYVALNKRGKAKRGCSPRVKPQHISTHFLPRFKQSEQPELS 228

Qy     169 FNTPIPRR 176

Db     229 FTVTVPEK 236


RESULT 12
FGF3_CHICK
ID   FGF3_CHICK     STANDARD;      PRT;   220 AA.
AC   P48801;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).
GN   FGF3 OR FGF-3.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rhode Island red; TISSUE=Embryo;
RX   MEDLINE=95309122; PubMed=7789270;
RA   Mahmood R., Kiefer P., Guthrie S., Dickson C., Mason I.;
RT   "Multiple roles for FGF-3 during cranial neural development in the
RT   chicken.";
RL   Development 121:1399-1410(1995).
CC   -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z47555; CAA87635.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Mitogen; Signal; Glycoprotein.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    220       FIBROBLAST GROWTH FACTOR-3.
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   220 AA;  25050 MW;  B15D41D1E551C5D5 CRC64;

  Query Match           12.3%;  Score 167;  DB 1;  Length 220;
  Best Local Similarity  33.3%;  Pred. No. 4.3e-08;
  Matches   49;  Conservative   18;  Mismatches   70;  Indels   10;  Gaps    4;

Qy       6 LRLW--VCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATAR------NSYHLQIHK 57

Db       2 LVIWLLLLALLPEPRVPAATASPRAPRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQIHP 61

Qy      58 NGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQ 116

Db      62 GGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLAMNKRGRLYASENYNTE-CEFV 120

Qy     117 HQTLENGYDVYHSPQYHFLVSLGRAKR 143

Db     121 ERIHELGYNTYASRLYRTVPSGASTKR 147


RESULT 13
FGF3_BRARE
ID   FGF3_BRARE     STANDARD;      PRT;   256 AA.
AC   P48802;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).
GN   FGF3 OR FGF-3.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96204005; PubMed=8622866;
RA   Kiefer P., Strahle U., Mason I., Dickson C.;
RT   "Secretion and mitogenic activity of zebrafish FGF3 reveal
RT   intermediate properties relative to mouse and Xenopus homologues.";
RL   Oncogene 12:1503-1511(1996).
CC   -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC   ----------------------------------------------------------------------
DR   EMBL; Z48714; CAA88596.1; -.
DR   HSSP; P09038; 1BFG.
DR   ZFIN; ZDB-GENE-980526-178; fgf3.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Mitogen; Signal; Glycoprotein.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    256       FIBROBLAST GROWTH FACTOR-3.
SQ   SEQUENCE   256 AA;  28923 MW;  CEBA1C72A170BBDC CRC64;

  Query Match           11.7%;  Score 159.5;  DB 1;  Length 256;
  Best Local Similarity  37.2%;  Pred. No. 2.5e-07;
  Matches   42;  Conservative   13;  Mismatches   39;  Indels   19;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRG 100

Db      66 LYCAT---KYHLQIHPNGKIDGSLEENNPLSILEITAVDVGVVAIKGLFSGRYLAMNEKG 122

Qy     101 NIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPP 153

Db     123 RLYASEVFNRE-CEFLERIHELGYNTYAS-RHHATT------------QPPP 160


RESULT 14
FGFB_XENLA
ID   FGFB_XENLA     STANDARD;      PRT;   192 AA.
AC   P48806;
DT   01-FEB-1996 (Rel. 33, Created)
```

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DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-4-II precursor (FGF-4-II) (HBGF-4-II)
DE   (Embryonic fibroblast growth factor II) (XEFGF-II).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92315916; PubMed=1618138;
RA   Isaacs H.V., Tannahill D., Slack J.M.W.;
RT   "Expression of a novel FGF in the Xenopus embryo. A new candidate
RT   inducing factor for mesoderm formation and anteroposterior
RT   specification.";
RL   Development 114:711-720(1992).
CC   -!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
CC       ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
CC       FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X62594; CAA44480.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Mitogen; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    192       FIBROBLAST GROWTH FACTOR-4-II.
SQ   SEQUENCE   192 AA;  21903 MW;  2B01B0BB8824E3B3 CRC64;

  Query Match             11.4%;  Score 155;  DB 1;  Length 192;
  Best Local Similarity   31.9%;  Pred. No. 4.4e-07;
  Matches   30;  Conservative   25;  Mismatches   37;  Indels    2;  Gaps    2;

Qy      51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
           :|:|:  :| ::|  ::  || | |   : | | : |: |  :: |: :| ::|| ||:
Db      80 FHIQVLPDGRINGMHNENRYSLLEISPVEVGVVSLYGIKSAMFVAMNAKGKLYGSRYFN- 138

Qy     111 ENCRFQHQTLENGYDVYHSPQY-HFLVSLGRAKR 143
           | |:|:   | | |: | | :|    ::||:  |
Db     139 EECKPKETLLPNNYNAYESRKYPGMYIALGKNGR 172


RESULT 15
FGFA_XENLA
ID   FGFA_XENLA     STANDARD;      PRT;   187 AA.
AC   P48805;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Fibroblast growth factor-4-I precursor (FGF-4-I) (HBGF-4-I) (Embryonic
DE   fibroblast growth factor I) (XEFGF-I).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92315916; PubMed=1618138;
RA   Isaacs H.V., Tannahill D., Slack J.M.W.;
RT   "Expression of a novel FGF in the Xenopus embryo. A new candidate
RT   inducing factor for mesoderm formation and anteroposterior
RT   specification.";
RL   Development 114:711-720(1992).
CC   -!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
CC       ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
CC       FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X62593; CAA44479.1; -.
DR   HSSP; P31371; 1G82.
DR   InterPro; IPR002209; HB/F_growthfact.
DR   InterPro; IPR002348; IL1_HBGF.
DR   Pfam; PF00167; FGF; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD000831; HB/F_growthfact; 1.
DR   SMART; SM00442; FGF; 1.
DR   PROSITE; PS00247; HBGF_FGF; 1.
KW   Growth factor; Mitogen; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    187       FIBROBLAST GROWTH FACTOR-4-I.
SQ   SEQUENCE   187 AA;  21223 MW;  AAE63D65E82AD1BD CRC64;

  Query Match             11.1%;  Score 151;  DB 1;  Length 187;
  Best Local Similarity   31.9%;  Pred. No. 9.8e-07;
  Matches   30;  Conservative   24;  Mismatches   38;  Indels    2;  Gaps    2;

Qy      51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
           :|:|:  :| ::|   :  || | :   : | | : || |  :: |: :| ::|| ||:
Db      75 FHIQVLPDGRINGMHSENRYSLLELSPVEVGVVSLYGVKSGMFVAMNAKGKLYGSRYFN- 133

Qy     111 ENCRFQHQTLENGYDVYHSPQY-HFLVSLGRAKR 143
           | |:|:   | | |: | | :|    ::||:  |
Db     134 EECKFKETLLPNNYNAYESRKYPGMYIALGKNGR 167


Search completed: May 23, 2003, 07:43:46
Job time : 26 secs
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 20 Seconds
(without alignments)
1206.487 Million cell updates/sec

Title: US-09-901-938-2
Perfect score: 1360
Sequence: 1 MLGARLRLWVCALCSVCSMS.....VNTHAGGTGPEGCRPFAKFI 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	961	70.7	251	2	JC7513	fibroblast growth
2	182.5	13.4	245	1	TVMST2	transforming prote
3	180.5	13.3	239	1	S04742	fibroblast growth
4	178.5	13.1	237	1	S39582	transforming prote
5	176.5	13.0	266	2	S68144	fibroblast growth
6	171	12.6	264	2	A36207	fibroblast growth
7	169	12.4	267	1	TVHUF5	fibroblast growth
8	167	12.3	220	2	I50588	fibroblast growth
9	159.5	11.7	256	2	JC4627	fibroblast growth
10	155	11.4	192	2	S54407	embryonic fibrobla
11	151	11.1	187	2	S23595	embryonic fibrobla
12	146.5	10.8	194	2	I50710	fibroblast growth
13	141.5	10.4	208	2	S20102	fibroblast growth
14	138.5	10.2	208	2	S14192	fibroblast growth
15	138	10.1	206	2	JC4268	fibroblast growth
16	132.5	9.7	211	2	JC7353	fibroblast growth
17	132	9.7	207	2	JC5940	fibroblast growth
18	131.5	9.7	206	1	TVHUHS	fibroblast growth
19	131	9.6	202	1	TVMSHS	fibroblast growth
20	130.5	9.6	212	2	JC7511	fibroblast growth
21	129	9.5	207	2	JC5941	fibroblast growth
22	128	9.4	194	2	S26049	fibroblast growth
23	128	9.4	194	2	I48610	keratinocyte growt
24	127	9.3	168	2	JG0184	fibroblast growth
25	127	9.3	194	2	S49501	keratinocyte growt
26	126	9.3	194	1	A36301	fibroblast growth
27	121.5	8.9	208	2	JC7082	fibroblast somatot
28	118	8.7	208	2	S66486	fibroblast growth
29	118	8.7	208	2	A48137	fibroblast growth
30	117	8.6	154	2	A31674	basic fibroblast g
31	116.5	8.6	154	2	C37360	basic fibroblast g
32	116.5	8.6	164	2	S31622	basic fibroblast g
33	115.5	8.5	137	2	I46711	fibroblast growth
34	115.5	8.5	146	1	S00185	basic fibroblast g
35	115.5	8.5	157	1	GKBOB	basic fibroblast g
36	115.5	8.5	210	2	A32398	basic fibroblast g
37	107.5	7.9	155	2	S04147	acidic fibroblast
38	107.5	7.9	155	2	D37360	acidic fibroblast
39	106.5	7.8	155	2	A60130	acidic fibroblast
40	105.5	7.8	155	1	A60721	acidic fibroblast
41	103	7.6	189	2	A48834	basic fibroblast g
42	101	7.4	155	1	GKBOA	acidic fibroblast
43	100	7.4	215	2	G02092	fibroblast growth
44	100	7.4	215	2	A46245	fibroblast growth
45	99.5	7.3	155	2	JW0055	acidic fiblobrast

ALIGNMENTS

RESULT 1
JC7513
fibroblast growth factor-23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7513
R;Yamashita, T.; Yoshioka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A;Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially ex
A;Reference number: JC7513; MUID:20490027; PMID:11032749
A;Contents: Embryo
A;Accession: JC7513
A;Molecule type: mRNA
A;Residues: 1-251 <YAM>
A;Cross-references: DDBJ:AB037889
C;Comment: This factor, a secreted protein, acts on proximal cells and plays roles in
C;Genetics:
A;Gene: fgf-23
C;Keywords: nucleus

Query Match 70.7%; Score 961; DB 2; Length 251;
Best Local Similarity 70.5%; Pred. No. 5.4e-80;
Matches 177; Conservative 25; Mismatches 49; Indels 0; Gaps 0;

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Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           |||  ||| |  ||:|||:   ||||: |||||:|| | |||||||| |||||||::||
Db       1 MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATARTSYHLQIHRDGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||| |||||||||||| ||||| ||||| |:||:|||| |||||| :| ||||:|:  ||
Db      61 VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHGNIFGSLHFSPENCKFRQWTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||| | ::|:|||||||||| | || ||||:||||:||||:||:|| |  |||||||
Db     121 ENGYDVYLSQKHHYLVSLGRAKRIFQPGTNPPPFSQFLARRNEVPLLHFYTVRPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           |||  |||||||||||| | || | |||:||||||:  | |||||||:|.|| :   |  |
Db     181 AEDPPERDPLNVLKPRPRATPVPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARGGAGG 240

Qy     241 PEGCRPFAKFI 251
             : |||| :|:
Db     241 ADRCRPFPRFV 251
```

RESULT 2
TVMST2
transforming protein (int-2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C;Accession: A23930; S08157
R;Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.

```
EMBO J. 5, 919-924, 1986
A;Title: Sequence, topography and protein coding potential of mouse int-2: a putative or
A;Reference number: A23930; MUID:86247582; PMID:3013624
A;Accession: A23930
A;Molecule type: DNA; mRNA
A;Residues: 1-245 <MOO>
A;Cross-references: GB:Y00848; GB:M26284; GB:X68450; NID:g52716; PIDN:CAA68767.1; PID:g5
R;Acland, P.; Dixon, M.; Peters, G.; Dickson, C.
Nature 343, 662-665, 1990
A;Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation
A;Reference number: S08157; MUID:90158795; PMID:2406607
A;Accession: S08157
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'HSRAGLARGRVLPAPRLRETRAGAAAAAGGRDAGM',3-17 <ACL>
C;Genetics:
A;Gene: int-2
A;Map position: 7
A;Introns: 74/1; 108/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein

  Query Match             13.4%;  Score 182.5;  DB 1;  Length 245;
  Best Local Similarity   29.4%;  Pred. No. 4.2e-09;
  Matches   63;  Conservative   26;  Mismatches   88;  Indels   37;  Gaps    8;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: || .
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152
           :: | ::: | | |  :  | ||: | | |   |   |:|   ||   |
Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNEIPLIHFNTPIPR-------RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
            |   | :|| :   :     :||          |  :    | |    :|| |
Db     162 RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR------ 211

Qy     205 SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
           |:  |  |: |  : |           | ||
Db     212 --RQKKQSPGDHGKM--ETLSTRATPSTQLHTGG 241


RESULT 3
S04742
fibroblast growth factor 3 precursor - human
N;Alternate names: transforming protein int-2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C;Accession: S04742
R;Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.
Oncogene 4, 429-436, 1989
A;Title: Sequence organization of the human int-2 gene and its expression in teratocarci
A;Reference number: S04742; MUID:89239468; PMID:2470007
A;Accession: S04742
A;Molecule type: DNA
A;Residues: 1-239 <BRO>
A;Cross-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1; PID:g312409
C;Genetics:
A;Gene: GDB:FGF3; INT2
A;Cross-references: GDB:120103; OMIM:164950
A;Map position: 11q13.3-11q13.3
A;Introns: 74/1; 108/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-239/Product: transforming protein (int-2) #status predicted <MAT>

  Query Match             13.3%;  Score 180.5;  DB 1;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 6.1e-09;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | | |  : |           |:| : :|     |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
           | :|| :   :     :  |     |  :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 4
S39582
transforming protein int-2 - African clawed frog
N;Alternate names: FGF-3 protein; fibroblast growth factor 3
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S39582; S25713
R;Kiefer, P.; Mathieu, M.; Close, M.J.; Peters, G.; Dickson, C.
EMBO J. 12, 4159-4168, 1993
A;Title: FGF3 from Xenopus laevis.
A;Reference number: S39582; MUID:94038898; PMID:8223431
A;Accession: S39582
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <KIE>
A;Cross-references: EMBL:Z25539; NID:g396830; PIDN:CAA80987.1; PID:g396831
R;Tannahill, D.; Isaacs, H.V.; Close, M.J.; Peters, G.; Slack, J.M.W.
Development 115, 695-702, 1992
A;Title: Developmental expression of the Xenopus int-2 (FGF-3) gene: activation by mes
A;Reference number: S25713; MUID:93048831; PMID:1425349
A;Accession: S25713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 39-137 <TAN>
A;Cross-references: EMBL:X65237; NID:g64855; PIDN:CAA46341.1; PID:g64856
C;Superfamily: fibroblast growth factor

  Query Match             13.1%;  Score 178.5;  DB 1;  Length 237;
  Best Local Similarity   32.2%;  Pred. No. 9.2e-09;
  Matches   55;  Conservative   26;  Mismatches   63;  Indels   27;  Gaps    8;

Qy      42 LYTATARNSYHLQIHKNGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRG 100
           || ||    |||||| || ::|     :::| | | : | | | | |: | ||| |: ||
Db      66 LYCAT---KYHLQIHLNGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLAMNQRG 122

Qy     101 NIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVS------LGRAKRAFLPGMNPP-- 152
           .  :: |  ::|| | |  :  | ||: | |  | : |          |:| :   :|
Db     123 RLYASETYNPE-CEFVERIHELGYNTYASRLYRTVPSGAGTKRKASAERLWYVSINGKGR 181

Qy     153 PYSQFLSRRNE-----IPLIHFN---TPIPRRHTRSAEDDSERDPLNVLKP 195
           |    | :|| :     :| :  |     :   || :   :|      :|||
Db     182 PRRGFKTRRTQKSSLFLPRVLDNKDHDAVRLFHTNAVYRES------ILKP 226


RESULT 5
S68144
fibroblast growth factor 5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68144
R;Hattori, Y.; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A;Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel t
A;Reference number: S68144; MUID:96201703; PMID:8611621
A;Accession: S68144
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-266 <HAT>
A;Cross-references: EMBL:D64085; NID:g992952; PIDN:BAA10966.1; PID:g992953
C;Superfamily: fibroblast growth factor
```

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  Query Match             13.0%;  Score 176.5;  DB 2;  Length 266;
  Best Local Similarity   28.2%;  Pred. No. 1.6e-08;
  Matches   58;  Conservative   34;  Mismatches   75;  Indels   39;  Gaps    8;

Qy      28 ASPLLGSSWGGLIH---LYTATARNS----------YHLQIHKNGHVDGAPHQTIYSALM 74
           |||  ||   |  |    :: : | :          :||||: :| |:|:   :: | |
Db      63 ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILE 120

Qy      75 IRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS----- 129
           | :   | | | || | ::| |  :| :  |  |  ::|:|: :  || |: | |
Db     121 IFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQENSYNTYASAIHRT 179

Qy     130 -----PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHFNTPIPRRHTRSA 181
                |  |   |:|||   | : |   |  || |  ::| | : |   :| :
Db     180 EKTGREWYVALNKRGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEK----- 234

Qy     182 EDDSERDPLNVLKPRARMTPAPASCS 207
           : |    ||:  ::|:  | |
Db     235 -----KKPPRPWKPKVPLSPSRRSPS 255


RESULT 6
A36207
fibroblast growth factor 5 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Mar-2000
C;Accession: A36207; B37360
R;Haub, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A;Title: Expression of the murine fibroblast growth factor 5 gene in the adult central n
A;Reference number: A36207; MUID:91045929; PMID:1700424
A;Accession: A36207
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-264 <HAU>
A;Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; PIDN:AAB02660.1; PID:g
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A;Reference number: A37360; MUID:90201563; PMID:2318343
A;Accession: B37360
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-264 <HEB>
A;Cross-references: GB:M30643; NID:g193294; PIDN:AAA96698.1; PID:g309238
C;Superfamily: fibroblast growth factor

  Query Match             12.6%;  Score 171;  DB 2;  Length 264;
  Best Local Similarity   27.9%;  Pred. No. 5.1e-08;
  Matches   57;  Conservative   35;  Mismatches   72;  Indels   40;  Gaps    9;

Qy      28 ASPLLGSSWGGLIH---LYTATARNS----------YHLQIHKNGHVDGAPHQTIYSALM 74
           |||  ||   |  |    :: : | :          :||||: :| |:|:   :: | |
Db      63 ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILE 120

Qy      75 IRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS----- 129
           | :   | | | || | ::| |  :| :  |  |  ::|:|: :  || |: | |
Db     121 IFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQENSYNTYASAIHRT 179

Qy     130 -----PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHFNTPIPRRHTRSA 181
                |  |   |:|||   | : |   |  || |  ::| | : |   :| :
Db     180 EKTGREWYVALNKRGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVP------- 232

Qy     182 EDDSERDPLNVLKP--RARMTPAP 203
             : ::  |:    |  : | :|:|
Db     233 --EKKKPPVKPKVPLSQPRRSPSP 254


RESULT 7
TVHUF5
fibroblast growth factor 5 - human
N;Alternate names: transforming protein FGF5
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 17-Mar-2000
C;Accession: A31194
R;Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A;Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth
A;Reference number: A31194; MUID:89096942; PMID:3211147
A;Accession: A31194
A;Molecule type: mRNA
A;Residues: 1-267 <ZHA>
A;Cross-references: GB:M23536; GB:M21617; NID:g182539; PIDN:AAB60699.1; PID:g182542
C;Genetics:
A;Gene: GDB:FGF5
A;Cross-references: GDB:119907; OMIM:165190
A;Map position: 4q21-4q21
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein

  Query Match             12.4%;  Score 169;  DB 1;  Length 267;
  Best Local Similarity   30.5%;  Pred. No. 7.9e-08;
  Matches   57;  Conservative   27;  Mismatches   75;  Indels   28;  Gaps    7;

Qy      15 SVCSMSVLRAYPNASPLLGSSWGGL---IHLYTATARN---------SYHLQIHKNGHVD 62
           |  | |   : | ||  |||   ||      ::  ||              :||||: :| |:
Db      52 SAMSSSSASSSPAAS--LGSQGSGLEQSSFQWSLGARTGSLYCRVGIGFHLQIYPDGKVN 109

Qy      63 GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLEN 122
           |:    : | | | :   | | | || | ::| |  :| :  |  |  ::|:|: :  ||
Db     110 GSHEANMLSVLEIFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQEN 168

Qy     123 GYDVYHS----------PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHF 169
           |: | |            |  |   |:|||   |.: |   |  || |  ::| | : |
Db     169 SYNTYASAIHRTEKTGREWYVALNKRGKAKRGCSPRVKPQHISTHFLPRFKQSEQPELSF 228

Qy     170 NTPIPRR 176
              :| :
Db     229 TVTVPEK 235


RESULT 8
I50588
fibroblast growth factor 3 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C;Accession: I50588
R;Mahmood, R.; Kiefer, P.; Guthrie, S.; Dickson, C.; Mason, I.
Development 121, 1399-1410, 1995
A;Title: Multiple roles for FGF-3 during cranial neural development in the chicken.
A;Reference number: I50588; MUID:95309122; PMID:7789270
A;Accession: I50588
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-220 <MAH>
A;Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216
C;Superfamily: fibroblast growth factor

  Query Match             12.3%;  Score 167;  DB 2;  Length 220;
  Best Local Similarity   33.3%;  Pred. No. 9.3e-08;
  Matches   49;  Conservative   18;  Mismatches   70;  Indels   10;  Gaps    4;

Qy       6 LRLW--VCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATAR------NSYHLQIHK 57
           | :|  : ||     :    | | |    |   |   ||  | |         ||||||
Db       2 LVIWLLLLALLPEPRVPAATASPRAPRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQIHP 61

Qy      58 NGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQ 116
           | ::|     :::| | | : | | | | | |: | ||| |: || :: |   :: | | |
Db      62 GGKINGTLEKNSVPSILEITAVDVGIVAIKGLFSGRYLAMNKRGRLYASENYNTE-CEFV 120

Qy     117 HQTLENGYDVYHSPQYHFLVSLGRAKR 143
             :  | ||: | |  |  : |     ||
Db     121 ERIHELGYNTYASRLYRTVPSGASTKR 147


RESULT 9
```

JC4627
fibroblast growth factor 3 - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
C;Accession: JC4627
R;Kiefer, P.; Straehle, U.; Dickson, C.
Gene 168, 211-215, 1996
A;Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic organ
A;Reference number: JC4627; MUID:96194899; PMID:8654946
A;Accession: JC4627
A;Molecule type: mRNA
A;Residues: 1-256 <KIE>
A;Cross-references: EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g971334
A;Experimental source: embryo
A;Note: The authors translated the codon TGG for residue 178 as His
C;Comment: This factor belongs to the fibroblast growth factor family which have the fun
otein is a cell signalling molecule and plays the roles during the early stages of devel
C;Genetics:
A;Gene: Fgf-3
A;Introns: 93/2; 127/3
C;Superfamily: fibroblast growth factor
C;Keywords: embryo; fibroblast; growth factor

Query Match 11.7%; Score 159.5; DB 2; Length 256;
Best Local Similarity 37.2%; Pred. No. 5.5e-07;
Matches 42; Conservative 13; Mismatches 39; Indels 19; Gaps 5;

Qy 42 LYTATARNSYHLQIHKNGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRG 100
Db 66 LYCAT---KYHLQIHPNGKIDGSLEENNPLSILEITAVDVGVVAIKGLFSGRYLAMNEKG 122

Qy 101 NIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPP 153
Db 123 RLYASEVFNRE-CEFLERIHELGYNTYAS-RHHATT----------QPPP 160

RESULT 10
S54407
embryonic fibroblast growth factor II - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S54407
R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
Development 114, 711-720, 1992
A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing facto
A;Reference number: S23595; MUID:92315916; PMID:1618138
A;Accession: S54407
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <ISA>
A;Cross-references: EMBL:X62594; NID:g840919; PIDN:CAA44480.1; PID:g840920
C;Superfamily: fibroblast growth factor

Query Match 11.4%; Score 155; DB 2; Length 192;
Best Local Similarity 31.9%; Pred. No. 9.7e-07;
Matches 30; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

Qy 51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
Db 80 FHIQVLPDGRINGMHNENRYSLLEISPVEVGVVSLYGIKSAMFVAMNAKGKLYGSRYFN- 138

Qy 111 ENCRFQHQTLENGYDVYHSPQY-HFLVSLGRAKR 143
Db 139 EECKFKETLLPNNYNAYESRKYPGMYIALGKNGR 172

RESULT 11
S23595
embryonic fibroblast growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S23595
R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
Development 114, 711-720, 1992
A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fac
A;Reference number: S23595; MUID:92315916; PMID:1618138
A;Accession: S23595
A;Molecule type: mRNA
A;Residues: 1-187 <ISA>
A;Cross-references: EMBL:X62593; NID:g64692; PIDN:CAA44479.1; PID:g64693
C;Superfamily: fibroblast growth factor

Query Match 11.1%; Score 151; DB 2; Length 187;
Best Local Similarity 31.9%; Pred. No. 2.2e-06;
Matches 30; Conservative 24; Mismatches 38; Indels 2; Gaps 2;

Qy 51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
Db 75 FHIQVLPDGRINGMHSENRYSLLELSPVEVGVVSLYGVKSGMFVAMNAKGKLYGSRYFN- 133

Qy 111 ENCRFQHQTLENGYDVYHSPQY-HFLVSLGRAKR 143
Db 134 EECKFKETLLPNNYNAYESRKYPGMYIALGKNGR 167

RESULT 12
I50710
fibroblast growth factor 4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: S78506; S50858; I50710
R;Niswander, L.
submitted to the EMBL Data Library, September 1994
A;Reference number: S78506
A;Accession: S78506
A;Molecule type: DNA
A;Residues: 1-194 <NIS>
A;Cross-references: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
R;Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
Nature 371, 609-612, 1994
A;Title: A positive feedback loop coordinates growth and patterning in the vertebrate
A;Reference number: I50710; MUID:95021713; PMID:7935794
A;Accession: S50858
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136,'Q',137-194,'I' <NIW>
A;Cross-references: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
C;Genetics:
A;Gene: FGF4
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein

Query Match 10.8%; Score 146.5; DB 2; Length 194;
Best Local Similarity 31.1%; Pred. No. 5.9e-06;
Matches 51; Conservative 22; Mismatches 68; Indels 23; Gaps 7;

Qy 3 GARLRLWVCALC--SVCSMSVLR--AYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKN 58
Db 33 GPRQRRWDAALFARSVARLPAERRDAARDGDYLLG--YKRLRRLY-CNVGIGFHIQVLPD 89

Qy 59 GHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQ 118
Db 90 GRIDGIHSENRYSLLEISPVERGVVSIFGVRSGLFVAMNSKGKLYGSTHVNDE-CKFKEI 148

Qy 119 TLENGYDVYHS----PQYHFLVSLGRAKRA----------FLP 147
Db 149 LLPNNYNAYESRIYPGMYIALSKNGRTKKGNKVSPTMTVTHFLP 192

RESULT 13
S20102
fibroblast growth factor 6 precursor - human
N;Alternate names: fibroblast growth factor-related protein FGF.6; transforming protei
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 21-Jul-2000
C;Accession: S20102; S23739; S04204; S36910

R;Coulier, F.; Batoz, M.; Marics, I.; de Lapeyriere, O.; Birnbaum, D.
Oncogene 6, 1437-1444, 1991
A;Title: Putative structure of the FGF6 gene product and role of the signal peptide.
A;Reference number: S20102; MUID:91360279; PMID:1886714
A;Accession: S20102
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-208 <COU>
A;Cross-references: EMBL:X57075
A;Note: it is uncertain whether Met-1, Met-11 or Met-34 is the initiator
R;Iida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Sato, T.; Or
Oncogene 7, 303-309, 1992
A;Title: Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.
A;Reference number: S23739; MUID:92195660; PMID:1549352
A;Accession: S23739
A;Molecule type: mRNA
A;Residues: 1-208 <IID>
A;Cross-references: EMBL:X63454
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;Marics, I.; Adelaide, J.; Raybaud, F.; Mattei, M.G.; Coulier, F.; Planche, J.; de Lape
Oncogene 4, 335-340, 1989
A;Title: Characterization of the HST-related FGF.6 gene, a new member of the fibroblast
A;Reference number: S04204; MUID:89201880; PMID:2649847
A;Accession: S04204
A;Molecule type: DNA
A;Residues: 81-99,'G',101-208 <MAR>
A;Cross-references: EMBL:X14071; NID:g31354; PIDN:CAB37648.2; PID:g4467836
C;Genetics:
A;Gene: GDB:FGF6; hst-2
A;Cross-references: GDB:119908; OMIM:134921
A;Map position: 12p13-12p13
A;Introns: 115/3; 150/2
C;Superfamily: fibroblast growth factor
F;1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted <SIG>
F;41-208/Product: fibroblast growth factor 6 #status predicted <MAT>

  Query Match 10.4%; Score 141.5; DB 2; Length 208;
  Best Local Similarity 28.7%; Pred. No. 1.8e-05;
  Matches 41; Conservative 21; Mismatches 56; Indels 25; Gaps 6;

```
Qy      28 ASPLLGSSW--GGLI------HLYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSED 79
           |  : | :|  | |:        ||       :|||:  :| : |   :  || | | : :
Db      66 AGEIAGVNWESGYLVGIKRQRRLY-CNVGIGFHLQVLPDGRISGTHEENPYSLLEISTVE 124

Qy      80 AGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYH----FL 135
           | | : || |  :: |: :| :: :  |  | |:|:   | | |: | |  |      |
Db     125 RGVVSLFGVRSALFVAMNSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLYQGTYIAL 183

Qy     136 VSLGRAKRA-----------FLP 147
           || ||             |||
Db     184 SKYGRVKRGSKVSPIMTVTHFLP 206
```

RESULT 14
S14192
fibroblast growth factor 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S14192; I49665; I49664
R;de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche, J.
Oncogene 5, 823-831, 1990
A;Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
A;Reference number: S14192; MUID:90295275; PMID:2193291
A;Accession: S14192
A;Molecule type: DNA
A;Residues: 1-208 <LAP>
A;Cross-references: EMBL:X51552
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;Ollendorff, V.; Rosnet, O.; Marics, I.; Birnbaum, D.; deLapeyriere, O.
Biochimie 74, 1035-1038, 1992
A;Title: Isolation and sequence of the murine Fgf6 cDNA.
A;Reference number: I49664; MUID:93120244; PMID:1477139
A;Accession: I49665
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 19-208 <RES>
A;Cross-references: GB:M92416; NID:g193288; PIDN:AAA62261.1; PID:g666915
A;Accession: I49664
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18 <RE2>
A;Cross-references: GB:M92415; NID:g193286; PIDN:AAA62260.1; PID:g193287
C;Genetics:
A;Gene: Fgf6
A;Introns: 116/1; 150/3
C;Superfamily: fibroblast growth factor

  Query Match 10.2%; Score 138.5; DB 2; Length 208;
  Best Local Similarity 28.7%; Pred. No. 3.4e-05;
  Matches 41; Conservative 21; Mismatches 56; Indels 25; Gaps 6;

```
Qy      28 ASPLLGSSW--GGLI------HLYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSED 79
           |  : | :|  | |:        ||       :|||:  :| : |   :  || | | : :
Db      66 AGEISGVNWESGYLVGIKRQRRLY-CNVGIGFHLQVPPDGRISGTHEENPYSLLEISTVE 124

Qy      80 AGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYH----FL 135
           | | : || |  :: |: :| :: :  |  | |:|:   | | |: | |  |      |
Db     125 RGVVSLFGVKSALFIAMNSKGRLYTTPSFHDE-CKFRETLLPNNYNAYESDLYRGTYIAL 183

Qy     136 VSLGRAKRA-----------FLP 147
           || ||             |||
Db     184 SKYGRVKRGSKVSPIMTVTHFLP 206
```

RESULT 15
JC4268
fibroblast growth factor 4 - bovine
N;Alternate names: transforming protein hst
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C;Accession: JC4268
R;Yu, J.C.; DeSeabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heidara
Gene 162, 333-334, 1995
A;Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A;Reference number: JC4268; MUID:96032369; PMID:7557455
A;Accession: JC4268
A;Molecule type: mRNA
A;Residues: 1-206 <YUJ>
A;Cross-references: GB:U15969
A;Note: The authors translated the codon GGC for residue 114 as Ser
C;Comment: This protein is a member of fibroblast growth factor family. The hstgene in
C;Genetics:
A;Gene: hst
A;Introns: 113/3; 145/2
C;Superfamily: fibroblast growth factor
C;Keywords: thymus; transforming protein

  Query Match 10.1%; Score 138; DB 2; Length 206;
  Best Local Similarity 32.1%; Pred. No. 3.8e-05;
  Matches 36; Conservative 16; Mismatches 44; Indels 16; Gaps 3;

```
Qy      51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
           :|||:  :| : |    |   | :   : | | | || || :: |  || ::|| :|
Db      94 FHLQVLPDGRIGGVHADTSDGLLELSPVERGVVSIFGVASRFFVAMSSRGRLYGSPFFTD 153

Qy     111 ENCRFQHQTLENGYDVY----HSPQYHFLVSLGRAKRA-----------FLP 147
           | |||:   | | |: |    |   :  |   |:||:             |||
Db     154 E-CRFREILLPNNYNAYECDRHPGMFIALSKNGKAKKGNRVSPTMKVTHFLP 204
```

Search completed: May 23, 2003, 07:44:12
Job time : 21 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:43:22 ; Search time 734 Seconds
(without alignments)
33.913 Million cell updates/sec

Title: US-09-901-938-2
Perfect score: 1360
Sequence: 1 MLGARLRLWVCALCSVCSMS.....VNTHAGGTGPEGCRPFAKFI 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1360	100.0	251	9	US-09-901-938-2	Sequence 2, Appli
2	1360	100.0	251	9	US-09-992-598-511	Sequence 511, App
3	1360	100.0	251	9	US-09-989-293A-511	Sequence 511, App
4	1360	100.0	251	9	US-09-989-735-511	Sequence 511, App
5	1360	100.0	251	9	US-09-990-444-511	Sequence 511, App
6	1360	100.0	251	9	US-09-989-730-511	Sequence 511, App
7	1360	100.0	251	9	US-09-990-436-511	Sequence 511, App
8	1360	100.0	251	9	US-09-991-181-511	Sequence 511, App
9	1360	100.0	251	9	US-09-993-687-511	Sequence 511, App
10	1360	100.0	251	9	US-09-989-734-511	Sequence 511, App
11	1360	100.0	251	9	US-10-028-072-266	Sequence 266, App
12	1360	100.0	251	9	US-09-997-653-511	Sequence 511, App
13	1360	100.0	251	9	US-09-993-667-511	Sequence 511, App
14	1360	100.0	251	9	US-10-121-049-266	Sequence 266, App
15	1360	100.0	251	9	US-10-123-904-266	Sequence 266, App
16	1360	100.0	251	9	US-10-140-470-266	Sequence 266, App
17	1360	100.0	251	9	US-09-924-340-26	Sequence 26, Appl
18	1360	100.0	251	9	US-09-990-438-511	Sequence 511, App
19	1360	100.0	251	9	US-09-990-562-511	Sequence 511, App
20	1360	100.0	251	9	US-09-992-600A-26	Sequence 26, Appl
21	1360	100.0	251	9	US-09-997-428-511	Sequence 511, App
22	1360	100.0	251	9	US-09-997-666-511	Sequence 511, App
23	1360	100.0	251	9	US-10-175-746-266	Sequence 266, App
24	1360	100.0	251	9	US-10-176-918-266	Sequence 266, App
25	1360	100.0	251	9	US-10-176-921-266	Sequence 266, App
26	1360	100.0	251	9	US-09-990-711-511	Sequence 511, App
27	1360	100.0	251	9	US-10-137-865-266	Sequence 266, App
28	1360	100.0	251	9	US-10-140-474-266	Sequence 266, App
29	1360	100.0	251	9	US-10-142-431-266	Sequence 266, App
30	1360	100.0	251	9	US-10-143-114-266	Sequence 266, App
31	1360	100.0	251	9	US-09-989-726-511	Sequence 511, App
32	1360	100.0	251	9	US-10-140-002-266	Sequence 266, App
33	1360	100.0	251	9	US-09-990-437-511	Sequence 511, App
34	1360	100.0	251	9	US-09-998-156-511	Sequence 511, App
35	1360	100.0	251	9	US-10-142-419-266	Sequence 266, App
36	1360	100.0	251	9	US-09-991-157-511	Sequence 511, App
37	1360	100.0	251	9	US-09-991-172-511	Sequence 511, App
38	1360	100.0	251	9	US-09-997-514-511	Sequence 511, App
39	1360	100.0	251	9	US-09-997-573-511	Sequence 511, App
40	1360	100.0	251	9	US-10-123-262-266	Sequence 266, App
41	1360	100.0	251	9	US-10-142-423-266	Sequence 266, App
42	1360	100.0	251	9	US-09-990-443-511	Sequence 511, App
43	1360	100.0	251	9	US-09-990-726-511	Sequence 511, App
44	1360	100.0	251	9	US-09-997-559-511	Sequence 511, App
45	1360	100.0	251	9	US-09-997-601-511	Sequence 511, App

ALIGNMENTS

RESULT 1
US-09-901-938-2
; Sequence 2, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-938-2

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 511, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
;  CURRENT APPLICATION NUMBER: US/09/992,598
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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;  PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Db     241 PEGCRPFAKFI 251
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RESULT 3
US-09-989-293A-511
; Sequence 511, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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Query Match 100.0%; Score 1360; DB 9; Length 251;

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Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
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Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPPAKFI 251
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Db     241 PEGCRPPAKFI 251


RESULT 4
US-09-989-735-511
; Sequence 511, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C61
;  CURRENT APPLICATION NUMBER: US/09/989,735
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/065186
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;  PRIOR APPLICATION NUMBER: 60/065311
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;  PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089600
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
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Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
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Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
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Db     241 PEGCRPFAKFI 251
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RESULT 5
US-09-990-444-511
; Sequence 511, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Qy     241 PEGCRPFAKFI 251
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Db     241 PEGCRPFAKFI 251
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RESULT 6
US-09-989-730-511
; Sequence 511, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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RESULT 7
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; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     241 PEGCRPFAKFI 251
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RESULT 8
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Db    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy    241 PEGCRPFAKFI 251
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RESULT 9
US-09-993-687-511
; Sequence 511, Application US/09993687
; Publication No. US20020198149A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; APPLICANT: Grimaldi,J.Christopher
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
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Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
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Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
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Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
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Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
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RESULT 11
US-10-028-072-266
; Sequence 266, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     241 PEGCRPFAKFI 251
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RESULT 12
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; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C4
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; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
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; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16

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; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
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; PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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RESULT 14
US-10-121-049-266
; Sequence 266, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 266
; LENGTH: 251
; TYPE: PRT

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;   ORGANISM: Homo Sapien
US-10-121-049-266

  Query Match            100.0%;  Score 1360;  DB 9;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-123;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
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; Sequence 266, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C54
;  CURRENT APPLICATION NUMBER: US/10/123,904
;  CURRENT FILING DATE:  2002-04-16
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 266
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-123-904-266

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  Best Local Similarity  100.0%;  Pred. No. 2.1e-123;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	182.5	13.4	245	1	US-08-439-725A-11	Sequence 11, Appl
2	182.5	13.4	245	2	US-08-867-471-11	Sequence 11, Appl
3	182.5	13.4	245	2	US-08-438-439C-7	Sequence 7, Appli
4	182	13.4	240	4	US-09-417-721-7	Sequence 7, Appli
5	180.5	13.3	239	1	US-08-464-590A-11	Sequence 11, Appl
6	180.5	13.3	239	1	US-08-462-169B-11	Sequence 11, Appl
7	180.5	13.3	239	2	US-08-207-412B-14	Sequence 14, Appl
8	180.5	13.3	239	2	US-08-951-822-35	Sequence 35, Appl
9	180.5	13.3	239	3	US-09-103-079-11	Sequence 11, Appl
10	180.5	13.3	239	3	US-08-718-904-12	Sequence 12, Appl
11	180.5	13.3	239	3	US-09-023-082A-21	Sequence 21, Appl
12	180.5	13.3	239	3	US-09-093-585-11	Sequence 11, Appl
13	180.5	13.3	239	4	US-09-368-951-35	Sequence 35, Appl
14	180.5	13.3	245	2	US-08-438-439C-17	Sequence 17, Appl
15	176	12.9	183	1	US-08-441-629-15	Sequence 15, Appl
16	176	12.9	183	3	US-08-776-207-15	Sequence 15, Appl
17	176	12.9	183	4	US-09-507-773-15	Sequence 15, Appl
18	176	12.9	183	5	PCT-US95-09172-15	Sequence 15, Appl
19	175.5	12.9	245	3	US-08-705-245-12	Sequence 12, Appl
20	174.5	12.8	266	4	US-09-417-721-9	Sequence 9, Appli
21	171	12.6	241	6	5175383-7	Patent No. 5175383
22	169	12.4	266	4	US-09-417-721-15	Sequence 15, Appl
23	169	12.4	267	1	US-08-462-169B-13	Sequence 13, Appl
24	169	12.4	267	3	US-09-103-079-13	Sequence 13, Appl
25	168.5	12.4	247	4	US-09-240-952-5	Sequence 5, Appli
26	168.5	12.4	248	4	US-09-240-952-3	Sequence 3, Appli
27	168.5	12.4	268	1	US-08-439-725A-12	Sequence 12, Appl
28	168.5	12.4	268	1	US-08-464-590A-17	Sequence 17, Appl
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32	168.5	12.4	268	2	US-08-951-822-33	Sequence 33, Appl
33	168.5	12.4	268	3	US-08-718-904-14	Sequence 14, Appl
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35	168.5	12.4	268	3	US-09-093-585-17	Sequence 17, Appl
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39	162	11.9	269	2	US-08-438-439C-18	Sequence 18, Appl
40	156	11.5	266	6	5175383-5	Patent No. 5175383
41	154	11.3	158	3	US-08-776-207-18	Sequence 18, Appl
42	154	11.3	158	4	US-09-507-773-18	Sequence 18, Appl
43	153.5	11.3	219	1	US-08-441-629-13	Sequence 13, Appl
44	153.5	11.3	219	3	US-08-776-207-13	Sequence 13, Appl
45	153.5	11.3	219	4	US-09-507-773-13	Sequence 13, Appl

ALIGNMENTS

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US-08-439-725A-11
; Sequence 11, Application US/08439725A
; Patent No. 5693775
;  GENERAL INFORMATION:
;    APPLICANT:  Nathans, Jeremy
;    APPLICANT:  Smallwood, Philip M.
;    APPLICANT:  Macke, Jennifer P.
;    TITLE OF INVENTION:  FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
;    TITLE OF INVENTION:  FACTOR-1 (FHF-1) AND METHODS OF USE
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/439,725A
;      FILING DATE:  12-MAY-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/047001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  617/678-5099
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  245 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-439-725A-11

  Query Match           13.4%;  Score 182.5;  DB 1;  Length 245;
  Best Local Similarity  29.4%;  Pred. No. 6.7e-12;
  Matches   63;  Conservative   26;  Mismatches   88;  Indels   37;  Gaps    8;

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RESULT 2
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; Patent No. 5872226
;  GENERAL INFORMATION:
;    APPLICANT:  Nathans, Jeremy
;    APPLICANT:  Smallwood, Philip M.
;    APPLICANT:  Macke, Jennifer P.
;    TITLE OF INVENTION:  FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
;    TITLE OF INVENTION:  FACTOR-1 (FHF-1) AND METHODS OF USE
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/867,471
;      FILING DATE:  02-JUN-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/439,725
;      FILING DATE:  12-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/047001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  617/678-5099
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  245 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-867-471-11

  Query Match             13.4%;  Score 182.5;  DB 2;  Length 245;
  Best Local Similarity   29.4%;  Pred. No. 6.7e-12;
  Matches   63;  Conservative   26;  Mismatches   88;  Indels   37;  Gaps    8;

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Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNEIPLIHFNTPIPR-------RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
            |   | :|| :   :     :||           |  :    | |    :|| |
Db     162 RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR------ 211

Qy     205 SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
             |:  |  |:  |  : |          | ||
Db     212 --RQKKQSPGDHGKM--ETLSTRATPSTQLHTGG 241


RESULT 3
US-08-438-439C-7
; Sequence 7, Application US/08438439C
; Patent No. 5876967
;  GENERAL INFORMATION:
;    APPLICANT:  Nathans, Jeremy
;    APPLICANT:  Smallwood, Phillip M.
;    APPLICANT:  Macke, Jennifer P.
;    TITLE OF INVENTION:  FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
;    TITLE OF INVENTION:  FACTOR-2 AND METHODS OF USE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,439C
;      FILING DATE:  May 12, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/046001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  245 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-438-439C-7

  Query Match             13.4%;  Score 182.5;  DB 2;  Length 245;
  Best Local Similarity   29.4%;  Pred. No. 6.7e-12;
  Matches   63;  Conservative   26;  Mismatches   88;  Indels   37;  Gaps    8;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152
           :: | ::: | | |  :  | ||: | |  |    |   |:|   ||   |
Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNEIPLIHFNTPIPR-------RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
            |   | :|| :   :     :||           |  :    | |    :|| |
Db     162 RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR------ 211

Qy     205 SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
             |:  |  |:  |  : |          | ||
Db     212 --RQKKQSPGDHGKM--ETLSTRATPSTQLHTGG 241


RESULT 4
```

```
US-09-417-721-7
; Sequence 7, Application US/09417721
; Patent No. 6451303
; GENERAL INFORMATION:
;  APPLICANT: Whitehouse, Martha J.
;  APPLICANT:  Kavanaugh, Michael W.
;  TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
;  TITLE OF INVENTION:  Administering
;  FILE REFERENCE: 1296/12169US05
;  CURRENT APPLICATION NUMBER: US/09/417,721
;  CURRENT FILING DATE:  1999-10-13
;  PRIOR APPLICATION NUMBER: 60/104,103
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Murine FGF-3
US-09-417-721-7

  Query Match             13.4%;  Score 182;  DB 4;  Length 240;
  Best Local Similarity   28.7%;  Pred. No. 7.4e-12;
  Matches   56;  Conservative   28;  Mismatches   69;  Indels   42;  Gaps    7;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | |: | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152
           :: | ::: | | |   :  | ||: | |  |     |   |:|   ||   |
Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNE----------------IPLIHFNTP-------IPRRHTRSAEDDSER 187
            |    | :|| :                : |:  : |         ||:  :   :   :
Db     162 RPRRGFKTRRTQKSSLFLPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQRRQKKQSPGDH 221

Qy     188 DPLNVLKPRARMTPA 202
             :  |  ||  ||:
Db     222 GKMETLSTRA--TPS 234


RESULT 5
US-08-464-590A-11
; Sequence 11, Application US/08464590A
; Patent No. 5763214
;  GENERAL INFORMATION:
;    APPLICANT:  HU, JING-SHAN
;    APPLICANT:  ROSEN, CRAIG A.
;    TITLE OF INVENTION:  FIBROBLAST GROWTH FACTOR-11
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,590A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J. G.
;      REGISTRATION NUMBER:  30,073
;      REFERENCE/DOCKET NUMBER:  325800-438
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 994-1700
;      TELEFAX:  (201) 994-1744
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-590A-11

  Query Match             13.3%;  Score 180.5;  DB 1;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |          |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
                | :|| :   :     :  |     | :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 6
US-08-462-169B-11
; Sequence 11, Application US/08462169B
; Patent No. 5773252
;  GENERAL INFORMATION:
;    APPLICANT:  John Greene and Craig A. Rosen
;    TITLE OF INVENTION:  Fibroblast Growth Factor-15
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,169B
;      FILING DATE:  05 JUN 95
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-441 (PF203)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-462-169B-11

  Query Match             13.3%;  Score 180.5;  DB 1;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;
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```
Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
             | :|| :   :     :  |     |  :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 7
US-08-207-412B-14
; Sequence 14, Application US/08207412B
; Patent No. 5817485
;  GENERAL INFORMATION:
;    APPLICANT:  Hu, Jing-Shan
;    TITLE OF INVENTION:  Fibroblast Growth Factor-10
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/207,412B
;      FILING DATE:  08-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
; INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-207-412B-14

  Query Match             13.3%;  Score 180.5;  DB 2;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
             | :|| :   :     :  |     |  :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 8
US-08-951-822-35
; Sequence 35, Application US/08951822A
; Patent No. 5989866
; GENERAL INFORMATION:
;  APPLICANT: Deisher, Theresa A.
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT: Raymond, Fenella
;  APPLICANT: Bukowski, Thomas R.
;  APPLICANT: Holderman, Susan D.
;  APPLICANT: Hansen, Birgit
;  APPLICANT: Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL FGF HOMOLOGS
;  FILE REFERENCE: 96-20
;  CURRENT APPLICATION NUMBER: US/08/951,822A
;  CURRENT FILING DATE: 1997-10-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-951-822-35

  Query Match             13.3%;  Score 180.5;  DB 2;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
             | :|| :   :     :  |     |  :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 9
US-09-103-079-11
; Sequence 11, Application US/09103079A
; Patent No. 6013477
; GENERAL INFORMATION:
;  APPLICANT: Greene, John M.
;  APPLICANT: Rosen, Craig A.
;  TITLE OF INVENTION: Fibroblast Growth Factor 15
;  FILE REFERENCE: PF203D1
;  CURRENT APPLICATION NUMBER: US/09/103,079A
;  CURRENT FILING DATE: 1998-06-23
;  EARLIER APPLICATION NUMBER: 08/462,169
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-103-079-11

  Query Match             13.3%;  Score 180.5;  DB 3;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
```

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                  | :|| :    :      :  |      |  :    | |   ::|| |
Db    164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 10
US-08-718-904-12
; Sequence 12, Application US/08718904
; Patent No. 6037329
;  GENERAL INFORMATION:
;    APPLICANT:  Baird, J. Andrew
;    APPLICANT:  Chandler, Lois Ann
;    APPLICANT:  Sosnowski, Barbara A.
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
;    NUMBER OF SEQUENCES:  128
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/718,904
;      FILING DATE:  24-SEP-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6037329tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  760100.415C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "FGF-3"
US-08-718-904-12

  Query Match             13.3%;  Score 180.5;  DB 3;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
           :: | ::  | | |  :  | ||: | | |  : |          |:| :   :|    |
Db     105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy     154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
             | :|| :   :     :  |      | :    | |   ::|| |
Db     164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 11
US-09-023-082A-21
; Sequence 21, Application US/09023082A
; Patent No. 6077692
;  GENERAL INFORMATION:
;    APPLICANT:  RUBEN, STEVEN M.
;    APPLICANT:  JIMENEZ, PABLO
;    APPLICANT:  DUAN, D. ROXANNE
;    APPLICANT:  RAMPY, MARK A.
;    APPLICANT:  MENDRICK, DONNA
;    APPLICANT:  ZHANG, JUN
;    APPLICANT:  NI, JIAN
;    APPLICANT:  MOORE, PAUL A.
;    APPLICANT:  COLEMAN, TIMOTHY A.
;    APPLICANT:  GRUBER, JOACHIM R.
;    APPLICANT:  DILLON, PATRICK J.
;    APPLICANT:  GENTZ, REINER L.
;    TITLE OF INVENTION:  KERATINOCYTE GROWTH FACTOR-2
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE, NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,082A
;      FILING DATE:  13-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01790
;      FILING DATE:  14-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/461,195
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/023,852
;      FILING DATE:  13-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,045
;      FILING DATE:  28-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/862,432
;      FILING DATE:  23-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/910,875
;      FILING DATE:  13-AUG-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/055,561
;      FILING DATE:  13-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0360008/EKS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-09-023-082A-21

  Query Match             13.3%;  Score 180.5;  DB 3;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
```

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          :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db    105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy    154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
            | :|| :   :     :  |      |  :    | |   ::|| |
Db    164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 12
US-09-093-585-11
; Sequence 11, Application US/09093585
; Patent No. 6110893
;  GENERAL INFORMATION:
;    APPLICANT:  HU, JING-SHAN
;    APPLICANT:  ROSEN, CRAIG A.
;    TITLE OF INVENTION:  FIBROBLAST GROWTH FACTOR-11
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/093,585
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/464,590
;      FILING DATE:  05-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J. G.
;      REGISTRATION NUMBER:  30,073
;      REFERENCE/DOCKET NUMBER:  325800-438
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 994-1700
;      TELEFAX:  (201) 994-1744
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-093-585-11

  Query Match             13.3%;  Score 180.5;  DB 3;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy     42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
          || ||     ||||:| :|  |:|:   : || | | : : | | | |: | ||| |: ||
Db     48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy    102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
          :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db    105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy    154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
            | :|| :   :     :  |      |  :    | |   ::|| |
Db    164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 13
US-09-368-951-35
; Sequence 35, Application US/09368951
; Patent No. 6352971
; GENERAL INFORMATION:
;  APPLICANT: Deisher, Theresa A.
;  APPLICANT: Conklin, Darrell C.
;  APPLICANT: Raymond, Fenella
;  APPLICANT: Bukowski, Thomas R.
;  APPLICANT: Holderman, Susan D.
;  APPLICANT: Hansen, Birgit
;  APPLICANT: Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL FGF HOMOLOGS
;  FILE REFERENCE: 96-20
;  CURRENT APPLICATION NUMBER: US/09/368,951
;  CURRENT FILING DATE: 1999-08-05
;  EARLIER APPLICATION NUMBER: 08/951,822
;  EARLIER FILING DATE: 1997-10-16
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-368-951-35

  Query Match             13.3%;  Score 180.5;  DB 4;  Length 239;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   26;  Mismatches   75;  Indels   15;  Gaps    5;

Qy     42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
          || ||     ||||:| :|  |:|:   : || | | : : | | | |: | ||| |: ||
Db     48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

Qy    102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL------GRAKRAFLPGMNPP--P 153
          :: | ::  | | |  :  | ||: | |  |  : |         |:| :   :|    |
Db    105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163

Qy    154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
            | :|| :   :     :  |      |  :    | |   ::|| |
Db    164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211


RESULT 14
US-08-438-439C-17
; Sequence 17, Application US/08438439C
; Patent No. 5876967
;  GENERAL INFORMATION:
;    APPLICANT:  Nathans, Jeremy
;    APPLICANT:  Smallwood, Phillip M.
;    APPLICANT:  Macke, Jennifer P.
;    TITLE OF INVENTION:  FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
;    TITLE OF INVENTION:  FACTOR-2 AND METHODS OF USE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,439C
;      FILING DATE:  May 12, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/046001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
```

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;       TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  245 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-438-439C-17

  Query Match             13.3%;  Score 180.5;  DB 2;  Length 245;
  Best Local Similarity   28.0%;  Pred. No. 1.1e-11;
  Matches   70;  Conservative   29;  Mismatches  104;  Indels   47;  Gaps   10;

Qy      19 MSVLR-AYPNASP------LLGSSWGGLIHLYTATAR------NSYHLQIHKNGHVDGAP 65
           :|:|  :||   |         |   |   ||  |  |         ||||:| :| |:|:
Db       9 LSLLEPSYPTTGPGTRLRRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQLHPSGRVNGSL 68

Qy      66 HQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYD 125
             : || | | : : | | | |: | ||| |: || :: | ::: | | |  :  | ||:
Db      69 ENSAYSILEITAVEVGGVAIKGLFSGRYLAMNKRGRLYASDHYNAE-CEFVERIHELGYN 127

Qy     126 VYHSPQYHFLVSLGRAKRAFLPGMNPP----------PYSQFLSRRNEIPLIHFNTPIPR 175
           | | |    |   |:|   ||  |           |   | :|| :  :    :||
Db     128 TYASRLYRTGSSGPGAQRQ--PGAQRPYYVSVNGKGRPRRGFKTRRTQKSSLF----LPR 181

Qy     176 -------RHTRSAEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVR 228
                  |  :    | |    :|| |         |:  |  |:  |  : |
Db     182 VLGHKDHEMVRLLQSSQPRAPGEGSQPRQR--------RQKKQSPGDHGKM--ETLSTRA 231

Qy     229 GGRVNTHAGG 238
                | ||
Db     232 TPSTQLHTGG 241


RESULT 15
US-08-441-629-15
; Sequence 15, Application US/08441629
; Patent No. 5766923
;  GENERAL INFORMATION:
;    APPLICANT:  Kirschner, Marc W.
;    APPLICANT:  Kinoshita, No. 5766923iyuki
;    TITLE OF INVENTION:  RECEPTOR-LIGAND ASSAY
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,629
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/279,217
;      FILING DATE:  22-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  HU95-01A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  183 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-441-629-15

  Query Match             12.9%;  Score 176;  DB 1;  Length 183;
  Best Local Similarity   35.6%;  Pred. No. 2.2e-11;
  Matches   47;  Conservative   19;  Mismatches   50;  Indels   16;  Gaps    4;

Qy      42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
           || ||    ||||:| :| |:|:   : || | | : : | | | | |: | ||| |: ||
Db      48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104

Qy     102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP--------- 152
           :: | ::: | | |  :  | ||: | |  |    |  :|  ||   |
Db     105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161

Qy     153 -PYSQFLSRRNE 163
            |   | :|| :
Db     162 RPRRGFKTRRTQ 173


Search completed: May 23, 2003, 07:46:21
Job time : 31 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:48 ; Search time 75 Seconds
(without alignments)
445.945 Million cell updates/sec

Title: US-09-901-938-2
Perfect score: 1360
Sequence: 1 MLGARLRLWVCALCSVCSMS.....VNTHAGGTGPEGCRPFAKFI 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1360	100.0	251	22	AAE09459	Human sbgFGF-19b p
2	1360	100.0	251	22	AAB85810	Human fibroblast g
3	1360	100.0	251	22	AAG63944	Amino acid sequenc
4	1360	100.0	251	22	AAG63947	Amino acid sequenc
5	1360	100.0	251	22	AAU12304	Human PRO9828 poly
6	1360	100.0	251	22	AAB84652	Amino acid sequenc
7	1360	100.0	251	22	AAG89178	Human secreted pro
8	1360	100.0	251	22	AAB65297	Human PRO9828 prot
9	1360	100.0	251	23	ABB77581	Human FGF23 protei
10	1360	100.0	251	23	AAU79355	Human fibroblast g
11	1360	100.0	251	23	ABB06940	Human OST311 prote
12	1360	100.0	251	23	ABB08352	Human zFGF12 amino
13	1356	99.7	251	23	ABB77582	Human FGF23 mutant
14	1356	99.7	251	23	ABB77583	Human FGF23 mutant
15	1356	99.7	251	23	AAU79379	Human fibroblast g
16	1356	99.7	251	23	AAU79380	Human fibroblast g
17	1352	99.4	251	23	ABB77584	Human FGF23 mutant
18	1352	99.4	251	23	ABB77585	Human FGF23 mutant
19	1352	99.4	251	23	AAU79381	Human fibroblast g
20	1348	99.1	251	23	ABB77586	Human FGF23 mutant
21	1261	92.7	233	22	AAB85829	Human fibroblast g
22	1235	90.8	227	22	AAB85811	Human fibroblast g
23	1235	90.8	227	23	ABB06941	Human OST311 prote
24	1235	90.8	229	23	ABB06952	MK-OST311 protein
25	1235	90.8	248	23	ABB06951	His-OST311 protein
26	966	71.0	178	21	AAY85638	Human fibroblast g
27	966	71.0	178	21	AAY85639	Human fibroblast g
28	961	70.7	251	22	AAG63945	Amino acid sequenc
29	961	70.7	251	22	AAG63946	Amino acid sequenc
30	961	70.7	251	23	AAU79356	Mouse fibroblast g
31	913	67.1	177	21	AAY85637	Monkey fibroblast
32	853	62.7	155	23	ABB06942	Human OST311 prote
33	813	59.8	149	23	ABB81314	Human FGF23 core s
34	676	49.7	180	23	ABB06944	Mouse OST311 prote
35	382	28.1	72	23	ABB06943	Human OST311 prote
36	241	17.7	210	21	AAB18636	Amino acid sequenc
37	241	17.7	210	22	AAB68416	Amino acid sequenc
38	241	17.7	210	22	AAU00958	Murine Fibroblast
39	241	17.7	210	23	AAE24375	Human FGF-21 prote
40	239	17.6	208	23	AAU79290	Rat FGF-related pr
41	229	16.8	208	22	AAE05078	Human fibroblast g
42	229	16.8	208	23	AAU83630	Human PRO protein,
43	229	16.8	208	23	AAE17601	Human extracellula
44	228.5	16.8	209	22	AAB83951	Amino acid sequenc
45	228.5	16.8	209	22	AAB82351	Human JAFFA protei

ALIGNMENTS

RESULT 1
AAE09459
ID AAE09459 standard; Protein; 251 AA.
XX
AC AAE09459;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human sbgFGF-19b protein.
XX
KW Human; Alzheimer's disease; amyotrophic lateral sclerosis;
KW ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;
KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;
KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
KW sexual disorder; growth abnormality; infection; autoimmune disease;
KW rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
KW cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
KW diabetes mellitus; glomerulonephritis; renovascular hypertension;
KW cancer; vaccine; gene therapy; sbgFGF-19b gene.
XX
OS Homo sapiens.
XX
PN WO200160850-A1.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US04703.
XX
PR 14-FEB-2000; 2000US-0182172.
PR 29-FEB-2000; 2000US-0186084.
PR 18-APR-2000; 2000US-0198583.

```
PR   04-OCT-2000; 2000US-0237963.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Kabnick KS,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2001-536566/59.
DR   N-PSDB; AAD16366.
XX
PT   New secreted and membrane associated polypeptides for treating
PT   Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT   disorders, stroke, and asthma  -
XX
PS   Claim 1; Page 91; 94pp; English.
XX
CC   The present sequence is a human sbgFGF-19b protein,
CC   a secreted protein of the invention.
CC   The invention relates to secreted and membrane associated polypeptides
CC   and nucleic acid molecules encoding such polypeptides. Sequences of the
CC   invention are useful for treating diseases such as Alzheimer's disease,
CC   amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
CC   of the immune system, haematopoietic disease, inflammation, anxiety,
CC   schizophrenia, feeding disorders, anorexia, depression, social, sexual
CC   and rewarded behaviour, cardiovascular disease, sleep disorder, learning
CC   and memory alteration and altered immune response, seizure, migraine,
CC   cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
CC   of transsexuals, growth abnormalities, obesity, infections, autoimmune
CC   diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
CC   disorders associated with healthy maintenance of gastric mucosa and
CC   repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
CC   ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
CC   amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
CC   congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
CC   viral and non-viral hepatitis, type I and type II diabetes mellitus,
CC   glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
CC   paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
CC   invention are used to identify membrane bound and soluble receptors.
CC   They are also useful as vaccines for inducing an immunological response
CC   in a mammal. Polynucleotides of the invention are used in gene therapy.
CC   They are also valuable for chromosome localisation studies and tissue
CC   expression studies.
XX
SQ   Sequence   251 AA;

  Query Match            100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
          ||||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 2
AAB85810
ID   AAB85810 standard; Protein; 251 AA.
XX
AC   AAB85810;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Human fibroblast growth factor (FGF)-23.
XX
KW   Fibroblast growth factor; FGF; FGF-23; osteopathic; vulnerary; ADHR;
KW   hepatotropic; autosomal dominant hypophosphatemic rickets; human;
KW   angiogenesis; gene-therapy; liver disorder; antisense-therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /note= "signal peptide"
FT   Protein         25..251
FT                   /note= "specifically claimed mature protein"
XX
PN   WO200161007-A2.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-US04778.
XX
PR   15-FEB-2000; 2000US-0182442.
PR   20-APR-2000; 2000US-0198903.
PR   15-FEB-2001; 2001US-0748581.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Luethy R,  Yang R,  Suggs S,  Sarosi D;
XX
DR   WPI; 2001-514774/56.
DR   N-PSDB; AAH76317.
XX
PT   An isolated nucleic acid molecule encoding a fibroblast growth factor
PT   23 useful for treating autosomal dominant hypophosphatemic rickets -
XX
PS   Claim 15; Fig 1A-B; 158pp; English.
XX
CC   This represents a human fibroblast growth factor (FGF)-23 polypeptide.
CC   The DNA insert is contained in ATCC Deposit No. PTA-1617. FGF-23 can be
CC   expressed by standard recombinant methodology. The FGF-23 polypeptides,
CC   polynucleotides, modulators and antibodies are useful for treating,
CC   preventing, or ameliorating an FGF-23 polypeptide-related disease,
CC   condition or disorder especially autosomal dominant hypophosphatemic
CC   rickets (ADHR). They are also useful for diagnosing a pathological
CC   condition and for stimulating angiogenesis, promoting wound healing and
CC   treating disorders of the liver.
XX
SQ   Sequence   251 AA;

  Query Match            100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
```

```
Qy    241 PEGCRPFAKFI 251
          ||||||||||| 
Db    241 PEGCRPFAKFI 251
```

RESULT 3
AAG63944
ID AAG63944 standard; Protein; 251 AA.
XX
AC AAG63944;
XX
DT 29-OCT-2001 (first entry)
XX
DE Amino acid sequence of human fibroblast growth factor 23 (FGF-23).
XX
KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
KW congenital defect; fertility; abnormal growth; thymus function;
KW leukemia; lymphoma; autoimmune disease; proliferative disorder;
KW differentiation disorder; central nervous system disorder; infarction;
KW Parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation;
KW intestinal wound; motility disorder; absorption disorder; stroke;
KW congenital malformation; ischemic vascular disease; myocardial ischemia;
KW peripheral vascular disease; renal artery disease; bone disease;
KW musculoskeletal disease; skeletal myopathy; arthritis.
XX
OS Homo sapiens.
XX
PN WO200166596-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07469.
XX
PR 08-MAR-2000; 2000US-0187854.
PR 18-SEP-2000; 2000US-0233368.
PR 05-DEC-2000; 2000US-0251649.
XX
PA (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
PI Itoh N, Kavanaugh MW;
XX
DR WPI; 2001-522948/57.
DR N-PSDB; AAH75021.
XX
PT Isolated nucleic acids encoding the human and murine fibroblast growth
PT factor 23, useful in the treatment of a condition characterized by
PT inadequate function of placental cells (e.g. congenital defects) and
PT the thymus (e.g. leukemia) -
XX
PS Claim 12; Fig 3; 77pp; English.
XX
CC The present sequence represents fibroblast growth factor 23 (FGF-23).
CC Human FGF-23 polynucleotides and polypeptides are useful for treating
CC a patient suffering from traumatic injury or a condition characterized
CC by dysfunction of or injury to skin cells, a condition characterized by
CC inadequate function of placental cells (e.g. congenital defects,
CC fertility, or abnormal growth), a condition characterized by inadequate
CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
CC proliferative disorder of the thymus, or differentiation disorder of
CC the thymus), or a condition characterized by central nervous system
CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
CC FGF-23 polynucleotide and polypeptide are also useful in the treatment
CC of Crohn's disease, healing of intestinal wounds, ulcers, inflammation,
CC injuries and surgical anastomoses, motility and absorption disorders,
CC and congenital malformations of the intestine. They are also useful for
CC treating ischemic vascular diseases (e.g. myocardial ischemia/infarction,
CC peripheral vascular disease, renal artery disease, stroke) and
CC musculoskeletal disease characterized by loss of function, inadequate
CC function or death of skeletal muscle cells, bone cells or supporting
CC cells (e.g. skeletal myopathies, bone disease, or arthritis).
XX
SQ Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 22; Length 251;
Best Local Similarity 100.0%; Pred. No. 7.5e-131;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy    241 PEGCRPFAKFI 251
          ||||||||||| 
Db    241 PEGCRPFAKFI 251
```

RESULT 4
AAG63947
ID AAG63947 standard; Protein; 251 AA.
XX
AC AAG63947;
XX
DT 29-OCT-2001 (first entry)
XX
DE Amino acid sequence of human fibroblast growth factor 23 (FGF-23).
XX
KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
KW congenital defect; fertility; thymus; leukemia; lymphoma; injury;
KW autoimmune disease; proliferative disorder; differentiation disorder;
KW central nervous system disorder; Parkinson's disease; inflammation;
KW Alzheimer's disease; Crohn's disease; intestinal wound; stroke;
KW motility disorder; absorption disorder; intestinal malformation;
KW ischemic vascular disease; myocardial ischemia; myocardial infarction;
KW peripheral vascular disease; renal artery disease; skeletal myopathy;
KW musculoskeletal disease; skeletal muscle cell; bone disease; arthritis.
XX
OS Homo sapiens.
XX
PN WO200166595-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07468.
XX
PR 08-MAR-2000; 2000US-0187854.
PR 18-SEP-2000; 2000US-0233368.
PR 05-DEC-2000; 2000US-0251650.
XX
PA (CHIR) CHIRON CORP.
PA (KYOU) UNIV KYOTO.
XX
PI Itoh N, Kavanaugh MW;
XX
DR WPI; 2001-522947/57.
DR N-PSDB; AAH75033.
XX
PT Isolated nucleic acids encoding the human and murine fibroblast growth
PT factor 23, useful in the treatment of a condition characterized by
PT inadequate function of placental cells (e.g. congenital defects) and
PT the thymus (e.g. leukemia) -
XX
PS Claim 12; Fig 3; 77pp; English.
XX

```
CC   The present sequence represents fibroblast growth factor 23 (FGF-23).
CC   The human FGF-23 polynucleotide and polypeptide are useful for treating
CC   a patient suffering from traumatic injury or a condition characterized
CC   by dysfunction of or injury to skin cells, a condition characterized
CC   by inadequate function of placental cells (e.g. congenital defects,
CC   fertility, or abnormal growth), a condition characterized by inadequate
CC   function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
CC   proliferative disorder of the thymus, or differentiation disorder of
CC   the thymus), or a condition characterized by central nervous system
CC   disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
CC   FGF-23 polynucleotide and polypeptide are also useful in the
CC   treatment of Crohn's disease, healing of intestinal wounds, ulcers,
CC   inflammation, injuries and surgical anastomoses, motility and
CC   absorption disorders, and congenital malformations of the intestine.
CC   They are also useful for treating ischemic vascular diseases (e.g.
CC   myocardial ischemia/infarction, peripheral vascular disease, renal
CC   artery disease, stroke) and musculoskeletal disease characterized by
CC   loss of function, inadequate function or death of skeletal muscle cells,
CC   bone cells or supporting cells (e.g. skeletal myopathies, bone disease,
CC   or arthritis).
XX
SQ   Sequence   251 AA;

  Query Match             100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 5
AAU12304
ID   AAU12304 standard; Protein; 251 AA.
XX
AC   AAU12304;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO9828 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   10-NOV-2000; 2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21376.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical -
XX
PS   Claim 12; Fig 266; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence   251 AA;

  Query Match             100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
```

```
Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           ||||||||||||
Db     241 PEGCRPFAKFI 251
```

RESULT 6
AAB84652
ID AAB84652 standard; Protein; 251 AA.
XX
AC AAB84652;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of fibroblast growth factor homologue zFGF12.
XX
KW Fibroblast growth factor; FGF; zFGF12; chromosome 12; 12q.1.3;
KW neuronal cell; prostatic cell; pancreatic cell; haematopoietic cell;
KW hyperplasia; regeneration; diabetes; amylotrophic lateral sclerosis;
KW stroke; angiogenesis; wound healing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /note= "signal peptide"
FT Protein 25..251
FT /note= "mature protein"
XX
PN WO200149740-A1.
XX
PD 12-JUL-2001.
XX
PF 04-JAN-2001; 2001WO-US00238.
XX
PR 05-JAN-2000; 2000US-0478062.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC;
XX
DR WPI; 2001-418357/44.
DR N-PSDB; AAH28133.
XX
PT A fibroblast growth factor homolog polypeptide zFGF12 and the nucleic
PT acids that encode it, useful for preventing, diagnosing and controlling
PT e.g. diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis
PT and wound healing -
XX
PS Claim 4; Page 60-61; 66pp; English.
XX
CC The present sequence represents a human fibroblast growth factor (FGF)
CC homologue, designated zFGF12. The zFGF12 polypeptides contain a motif
CC (see AAB84654) that occurs in all known members of the FGF family, which
CC is unique to these proteins. This motif is highly conserved in all
CC members of the FGF family, however, zFGF12 appears to be unique in that
CC the conserved Glu is a His (residue 117) substituting a basic amino
CC acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped
CC to chromosome 12, location 12q.1.3. zFGF12 may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate FGF expression. Disorders and processes that may be
CC prevented, diagnosed, and treated include, for example proliferation
CC of neuronal, prostatic and pancreatic tissue cells, growth and
CC differentiation of haematopoietic cells, hyperplasia and regeneration,
CC diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis and
CC wound healing.
XX
SQ Sequence 251 AA;

```
  Query Match             100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           ||||||||||||
Db     241 PEGCRPFAKFI 251
```

RESULT 7
AAG89178
ID AAG89178 standard; Protein; 251 AA.
XX
AC AAG89178;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 298.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-IB01938.
XX
PR 08-DEC-1999; 99US-0169629.
PR 06-MAR-2000; 2000US-0187470.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
DR WPI; 2001-367870/38.
DR N-PSDB; AAH64781.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases -
XX
PS Claim 21; Page 828-829; 921pp; English.
XX
CC The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For

```
CC   example, they be used to treat disorders associated with decreased
CC   GENSET gene expression by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of GENSET or by supplementing
CC   the patients own production of GENSET polypeptides. Conversely,
CC   antisense nucleic acid molecules may be administered to down regulate
CC   GENSET expression by binding with the cells' own genes and preventing
CC   their expression. The sense and antisense nucleic acids may also be
CC   used as DNA probes in diagnostic assays to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples, and hence to
CC   determine which patients may be in need of restorative therapy.
CC   The GENSET polypeptides may be used as antigens in the production of
CC   antibodies and in assays to identify modulators (agonists and
CC   antagonists) of GENSET polypeptide expression and activity. The
CC   present sequence is a GENSET polypeptide of the invention.
XX
SQ   Sequence   251 AA;

  Query Match            100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy    241 PEGCRPFAKFI 251
          |||||||||||
Db    241 PEGCRPFAKFI 251


RESULT 8
AAB65297
ID   AAB65297 standard; Protein; 251 AA.
XX
AC   AAB65297;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO9828 protein sequence SEQ ID NO:511.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic;
KW   cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US08439.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   07-JUL-1999;   99US-0143048.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   17-AUG-1999;   99US-0149396.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   08-OCT-1999;   99US-0158663.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   02-MAR-2000; 2000WO-US05841.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   N-PSDB; AAF44266.
XX
PT   PRO polynucleotides used to produce polypeptides used to target
PT   bioactive molecules such as toxins, radiolabels or antibodies, to
PT   specific cells, to cause targeted cell death -
XX
PS   Claim 12; Fig 324; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC   can be used for targeted delivery of bioactive molecules, such as
CC   toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA
CC   and DNA. They may also be used to produce transgenic animals which are
CC   used to develop and screen therapeutically useful reagents. The PRO
CC   nucleotide and protein sequence can be used for tissue typing and in
CC   treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC   AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC   AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   251 AA;

  Query Match            100.0%;  Score 1360;  DB 22;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy    241 PEGCRPFAKFI 251
          |||||||||||
Db    241 PEGCRPFAKFI 251
```

```
RESULT 9
ABB77581
ID   ABB77581 standard; Protein; 251 AA.
XX
AC   ABB77581;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Human FGF23 protein SEQ ID NO 2.
XX
KW   Human; FGF23; haemostatic; hyperphosphataemia; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200252009-A1.
XX
PD   04-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-JP11482.
XX
PR   26-DEC-2000; 2000JP-0396316.
PR   29-MAY-2001; 2001JP-0161370.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Itoh H,  Fukushima N,  Saito H,  Kusano K;
XX
DR   WPI; 2002-508891/54.
DR   N-PSDB; ABN81575.
XX
PT   Human FGF23 protein mutant for lowering blood phosphorus level,
PT   applicable in gene therapy remedies for hyperphosphatemia -
XX
PS   Claim 1; Page 46-48; 64pp; Japanese.
XX
CC   The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)
CC   FGF23 and mutants FGF23 comprising an amino acid substitution of arginine
CC   at position 176 to glutamine and/or position 179 to glutamine or
CC   tryptophan. The mutants are generated by introducing the following base
CC   changes in the nucleic acid sequence: R176Q mutant is generated by
CC   G527A; R179Q is generated by G536A; and R179W is generated by C535T. The
CC   protein and encoding DNA are applicable in remedies for
CC   hyperphosphataemia, including gene therapy.
XX
SQ   Sequence   251 AA;

  Query Match             100.0%;  Score 1360;  DB 23;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
          |||||||||||
Db     241 PEGCRPFAKFI 251
```

```
RESULT 10
AAU79355
ID   AAU79355 standard; Protein; 251 AA.
XX
AC   AAU79355;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human fibroblast growth factor-23 (FGF23).
XX
KW   Fibroblast growth factor 23; FGF23; hypophosphataemic disorder;
KW   autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;
KW   X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia;
KW   TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH;
KW   hypophosphataemic bone disease; HBD; epidermal nevus syndrome;
KW   nephrolithiasis; hyperphosphataemic disorder; mild renal insufficiency;
KW   tumoural calcinosis; osteoporosis; dermatomyositis; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Signal_peptide
FT   Protein         25
FT                   /label= Mature_FGF23
FT                   /note= "Fibroblast growth factor 23"
FT   Cleavage-site   176..179
FT                   /label= Protease_cleavage_site
XX
PN   WO200208271-A1.
XX
PD   31-JAN-2002.
XX
PF   10-JUL-2001; 2001WO-US21738.
XX
PR   19-JUL-2000; 2000US-219137P.
XX
PA   (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
XX
PI   Econs M,  White K,  Strom TM,  Meitinger T;
XX
DR   WPI; 2002-329399/36.
DR   N-PSDB; ABK48318.
XX
PT   Novel fibroblast growth factor 23, and polynucleotides encoding the
PT   polypeptides, useful for treating hyperphosphataemic disorders such as
PT   mild renal insufficiency or tumoural calcinosis, or coronary artery
PT   disease  -
XX
PS   Claim 3; Fig 9; 130pp; English.
XX
CC   The invention describes an isolated polypeptide (I) comprising a
CC   fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
CC   homologue or fragment. (I) is useful for treatment of a hypophosphataemic
CC   disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
CC   X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic
CC   rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD),
CC   epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
CC   (TIO), and nephrolithiasis. (I) can also be used in treatment of a
CC   hyperphosphataemic disorder such as mild renal insufficiency and tumoural
CC   calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
CC   deposition of calcium and phosphate in the arteries or soft tissues of
CC   mammal, coronary  artery disease may also be treated using methods
CC   described in the invention. Preferably, the nucleic acid or the
CC   polypeptide comprises a mutation that confers increased stability on
CC   FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene
CC   therapy to treat diseased individuals. This is the amino acid sequence
CC   of the novel human fibroblast growth factor 23 (FGF23) studied in the
CC   invention.
XX
SQ   Sequence   251 AA;
```

```
  Query Match           100.0%;  Score 1360;  DB 23;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 11
ABB06940
ID   ABB06940 standard; Protein; 251 AA.
XX
AC   ABB06940;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Human OST311 protein sequence SEQ ID NO:2.
XX
KW   OST311; phosphoric acid metabolism; calcium metabolism; calcification;
KW   vitamin D metabolism; hypophosphataemia; phosphate transport; cytostatic;
KW   chromosome 12p13; osteopathic; nephrotropic; antihyperphosphataemic;
KW   phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
KW   bone formation abnormality; vitamin D resistance; Paget's disease;
KW   bone calcium deficiency; kidney disorder; kidney function deficiency;
KW   renal phosphate leakage; urinary tubule acidosis; Fanconi's disease.
XX
OS   Homo sapiens.
XX
PN   WO200214504-A1.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-JP06944.
XX
PR   11-AUG-2000; 2000JP-0245144.
PR   21-SEP-2000; 2000JP-0287684.
PR   22-DEC-2000; 2000JP-0391077.
PR   19-APR-2001; 2001JP-0121527.
XX
PA   (KIRI ) KIRIN BEER KK.
XX
PI   Yamashita T,  Shimada T,  Mizutani S,  Fukumoto S;
XX
DR   WPI; 2002-227350/28.
DR   N-PSDB; ABL50577.
XX
PT   Polypeptides useful for regulating phosphate transport and calcium
PT   metabolism and DNA encoding them for treatment of phosphate and calcium
PT   metabolism disorders, including bone formation abnormalities and kidney
PT   diseases -
XX
PS   Claim 1; Page 158-159; 221pp; Japanese.
XX
CC   The present invention describes DNA encoding a polypeptide having the
CC   activities of inhibiting hypophosphataemia, phosphate transport and
CC   calcification, and regulating vitamin D metabolism in vivo. The
CC   polypeptide is of human origin (designated OST311) which is localised to
CC   chromosome 12p13, or is derived from this by addition, deletion and/or
CC   substitution of one or more amino acid residues. OST311 has osteopathic,
CC   nephrotropic, antihyperphosphataemic and cytostatic activities. The
CC   OST311 polypeptide regulates phosphorus transport and calcium metabolism.
CC   OST311 sequences can be used for the treatment and diagnosis of skeletal
CC   disorders such as bone cancer, bone formation abnormalities, vitamin D
CC   resistance, osteoporosis, Paget's disease and bone calcium deficiency;
CC   kidney disorders such as kidney function deficiency, renal phosphate
CC   leakage, urinary tubule acidosis and Fanconi's disease. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence   251 AA;

  Query Match           100.0%;  Score 1360;  DB 23;  Length 251;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 12
ABB08352
ID   ABB08352 standard; Protein; 251 AA.
XX
AC   ABB08352;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human zFGF12 amino acid sequence.
XX
KW   zFGF12; human; fibroblast growth factor; FGF; vulnerary; chemotherapy;
KW   lung injury; epithelial cell; mesenchymal cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= secretory_signal_sequence
FT   Region          2..51
FT                   /label= beta-strand_1
FT   Region          3..59
FT                   /label= beta-strand_2
FT   Region          4..71
FT                   /label= beta-strand_3
FT   Region          5..81
FT                   /label= beta-strand_4
FT   Region          6..92
FT                   /label= beta-strand_5
FT   Region          7..99
FT                   /label= beta-strand_6
FT   Region          8..113
FT                   /label= beta-strand_7
FT   Region          9..123
FT                   /label= beta-strand_8
```

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FT   Region          10..134
FT                   /label= beta-strand_9
FT   Region          11..143
FT                   /label= beta-strand_10
FT   Protein         25..251
FT                   /label= mature_zFGF12
FT   Region          53
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          61
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          73
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          75
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          82..131
FT                   /note= "block of residues with a high percentage identity
FT                   to other members of the FGF family"
FT   Region          85
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          94
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          102
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          113..117
FT                   /label= FGF_family_motif"
FT                   /note= "does not conform exactly to the consesus sequence
FT                   (see ABB08354)"
FT   Region          115
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          127
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
FT   Region          136
FT                   /note= "residue critical to the beta-trefoil fold of
FT                   zFGF12"
XX
PN   US2001044525-A1.
XX
PD   22-NOV-2001.
XX
PF   04-JAN-2001; 2001US-0754634.
XX
PR   05-JAN-2000; 2000US-174582P.
XX
PA   (CONK/) CONKLIN D C.
XX
PI   Conklin DC;
XX
DR   WPI; 2002-105575/14.
DR   N-PSDB; ABA97195.
XX
PT   New fibroblast growth factor, designated zFGF12 is for promoting wound
PT   healing, protecting and stimulating epithelial cells after chemotherapy
PT   or radiation, and stimulating lung epithelial cells after premature
PT   birth or injury -
XX
PS   Claim 5; Fig 1; 34pp; English.
XX
CC   The invention relates to a fibroblast growth factor polypeptide,
CC   designated zFGF12, comprising a sequence at least 95 % identical to
CC   residues 25 to 251 of the 251 amino acid sequence, given in the
CC   specification. The activity of the fibroblast growth factor of the
CC   invention may be described as vulnerary. zFGF12 can be used to promote
CC   wound healing of the epidermis, to protect and promote recovery of
CC   epithelial cells in the gastrointestinal tract, small intestine and oral
CC   mucosa after chemotherapy or radiation, and to stimulate lung epithelial
CC   cells after lung injury or complications in neonates following premature
CC   birth. The polypeptide can also be used to modulate proliferation and
CC   function of epithelial cells of prostate, cornea, mammary and kidney
CC   tissue. The polypeptide is also useful to stimulate proliferation of
CC   cultured mesenchymal cells and to identify new family members. The
CC   current sequence represents the human zFGF12 amino acid sequence.
XX
SQ   Sequence   251 AA;

  Query Match             100.0%;  Score 1360;  DB 23;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-131;
  Matches  251;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 13
ABB77582
ID   ABB77582 standard; Protein; 251 AA.
XX
AC   ABB77582;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Human FGF23 mutant R176Q.
XX
KW   Human; FGF23; haemostatic; hyperphosphataemia; gene therapy; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 176
FT                   /note= "Wildtype Arg substituted by Gln"
XX
PN   WO200252009-A1.
XX
PD   04-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-JP11482.
XX
PR   26-DEC-2000; 2000JP-0396316.
PR   29-MAY-2001; 2001JP-0161370.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Itoh H,  Fukushima N,  Saito H,  Kusano K;
XX
DR   WPI; 2002-508891/54.
XX
PT   Human FGF23 protein mutant for lowering blood phosphorus level,
PT   applicable in gene therapy remedies for hyperphosphatemia -
XX
```

```
PS   Example 2; Page -; 64pp; Japanese.
XX
CC   The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)
CC   FGF23 and mutants FGF23 comprising an amino acid substitution of arginine
CC   at position 176 to glutamine and/or position 179 to glutamine or
CC   tryptophan. The mutants are generated by introducing the following base
CC   changes in the nucleic acid sequence: R176Q mutant is generated by
CC   G527A; R179Q is generated by G536A; and R179W is generated by C535T. The
CC   protein and encoding DNA are applicable in remedies for
CC   hyperphosphataemia, including gene therapy. The present sequence is that
CC   of a FGF23 mutant of the invention.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the wildtype human FGF23 sequence given as SEQ ID NO 2 in
CC   the sequence listing (ABB77581).
XX
SQ   Sequence   251 AA;

  Query Match             99.7%;  Score 1356;  DB 23;  Length 251;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-130;
  Matches  250;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRQHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 14
ABB77583
ID   ABB77583 standard; Protein; 251 AA.
XX
AC   ABB77583;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Human FGF23 mutant R179Q.
XX
KW   Human; FGF23; haemostatic; hyperphosphataemia; gene therapy; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 179
FT                   /note= "Wildtype Arg substituted by Gln"
XX
PN   WO200252009-A1.
XX
PD   04-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-JP11482.
XX
PR   26-DEC-2000; 2000JP-0396316.
PR   29-MAY-2001; 2001JP-0161370.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Itoh H,  Fukushima N,  Saito H,  Kusano K;
XX
DR   WPI; 2002-508891/54.
XX
PT   Human FGF23 protein mutant for lowering blood phosphorus level,
PT   applicable in gene therapy remedies for hyperphosphatemia -
XX
PS   Example 2; Page -; 64pp; Japanese.
XX
CC   The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)
CC   FGF23 and mutants FGF23 comprising an amino acid substitution of arginine
CC   at position 176 to glutamine and/or position 179 to glutamine or
CC   tryptophan. The mutants are generated by introducing the following base
CC   changes in the nucleic acid sequence: R176Q mutant is generated by
CC   G527A; R179Q is generated by G536A; and R179W is generated by C535T. The
CC   protein and encoding DNA are applicable in remedies for
CC   hyperphosphataemia, including gene therapy. The present sequence is that
CC   of a FGF23 mutant of the invention.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the wildtype human FGF23 sequence given as SEQ ID NO 2 in
CC   the sequence listing (ABB77581).
XX
SQ   Sequence   251 AA;

  Query Match             99.7%;  Score 1356;  DB 23;  Length 251;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-130;
  Matches  250;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTQS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251


RESULT 15
AAU79379
ID   AAU79379 standard; Protein; 251 AA.
XX
AC   AAU79379;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human fibroblast growth factor-23 (FGF23), R176Q mutant.
XX
KW   Fibroblast growth factor 23; FGF23; hypophosphataemic disorder;
KW   autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;
KW   X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia;
KW   TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH;
KW   hypophosphataemic bone disease; HBD; epidermal nevus syndrome;
KW   nephrolithiasis; hyperphosphataemic disorder; mild renal insufficiency;
KW   tumoural calcinosis; osteoporosis; dermatomyositis; human; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 176
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FT                   /note= "Wild type Arg substituted by Gln"
XX
PN   WO200208271-A1.
XX
PD   31-JAN-2002.
XX
PF   10-JUL-2001; 2001WO-US21738.
XX
PR   19-JUL-2000; 2000US-219137P.
XX
PA   (ADRE-) ADVANCED RES & TECHNOLOGY INST.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
XX
PI   Econs M,  White K,  Strom TM,  Meitinger T;
XX
DR   WPI; 2002-329399/36.
XX
PT   Novel fibroblast growth factor 23, and polynucleotides encoding the
PT   polypeptides, useful for treating hyperphosphataemic disorders such as
PT   mild renal insufficiency or tumoural calcinosis, or coronary artery
PT   disease  -
XX
PS   Example 1; Page -; 130pp; English.
XX
CC   The invention describes an isolated polypeptide (I) comprising a
CC   fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
CC   homologue or fragment. (I) is useful for treatment of a hypophosphataemic
CC   disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
CC   X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic
CC   rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD),
CC   epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
CC   (TIO), and nephrolithiasis. (I) can also be used in treatment of a
CC   hyperphosphataemic disorder such as mild renal insufficiency and tumoural
CC   calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
CC   deposition of calcium and phosphate in the arteries or soft tissues of
CC   mammal, coronary  artery disease may also be treated using methods
CC   described in the invention. Preferably, the nucleic acid or the
CC   polypeptide comprises a mutation that confers increased stability on
CC   FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene
CC   therapy to treat diseased individuals. This sequence represents a mutant
CC   of the novel human fibroblast growth factor 23 (FGF23) used to study
CC   residues in the predicted protease cleavage site.
CC   Note: This sequence does not appear in the specification but has been
CC   created from the wild type sequence shown in AAU79355 using information
CC   given in example 1 of the invention.
XX
SQ   Sequence   251 AA;

  Query Match             99.7%;  Score 1356;  DB 23;  Length 251;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-130;
  Matches  250;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60

Qy      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120

Qy     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db     121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRQHTRS 180

Qy     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240

Qy     241 PEGCRPFAKFI 251
           |||||||||||
Db     241 PEGCRPFAKFI 251
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Job time : 77 secs